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Minimum
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Maximum Match 100%
Listing first 45 summaries
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Perfect score:
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                                                                                                                                                                                                                                                                                                                                                                                                                     DB DB
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A_Geneseq_16Dec04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2001as:*
6: geneseqp2001as:*
7: geneseqp2001as:*
8: geneseqp2001as:*
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Gapop 10.0 ,
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Query
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                       ABG32454
ABG32456
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AAR30616
AAE20477
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AAY70064
AAY70066
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               AAR34468
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(without alignments)
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                                                                                                                                 Aar29852 HCV NS2-N
Aar34002 BK EZ/NS1
Aar20111 Non-A, no
Aar20091 Non-A, no
Aay06423 Non-A, no
Adj82984 Adenovect
Aay70064 Recombina
Aay70065 Recombina
Aay70066 Recombina
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Abg32456
Aar30616
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Aar34468
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Hepatitis
Hepatitis
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Hepatitis
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Hepatitis
Encoded b
Hepatitis
HCV polyp
               Hepatitis
Hepatitis
Hepatitis
Hepatitis
Hepatitis
Hepatitis
Polypepti
HCV-S1 fu
Encoded b
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ALIGNMENTS

RESULT 1 AAR29852 CCCCCCCCX 12-JUL-1991; 07-OCT-1991; 16-DEC-1991; EP518313-A2. transcriptase; cDNA; Clone; polypeptide; NS2-NS4; Hepatitis transcriptase; cDNA; primer; allele. 25-MAR-2003 26-APR-1993 AAR29852; AAR29852 standard; protein; 11-JUN-1991; 11-JUN-1992; 16-DEC-1992 Hepatitis C virus. HCV NS2-NS4 peptide MX25-2. (revised) (first entry) 91JP-00139268. 91JP-00172794. 91JP-00287008. 91JP-00332329. 92EP-00109812 283 ₿ ü Virus; HCV; serum; HC;

The sequences given in AAR29852-70 are encodeed by various clones which were used in the isolation of the NS2-NS4 regions of the Hepatitis C Virus (HCV) gene of the invention (see also AAR29660, AAR29559-60 and AAR29843-51). These RNA sequences were isolated from the serum of a patient suffering from hepatitis C (HC). The isolated RNA sequences were converted into cDNA using transcriptase in the presence of one of the primer sequences given in AAQ32578-79. The sequences were then amplified using primer pairs. The cDNA sequences isolated represent different

WPI; 199 N-PSDB;

1992-417213/51. DB; AAQ32483.

Seki M,

Honda Y,

Takahashi K,

Murakami

H,

Teranishi

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Hayashi

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(MITU)

MITSUBISHI KASEI CORP.

92JP-00099957

New and

hepatitis C virus gene and its encoded protein - used vaccinating against hepatitis C virus infections.

for

diagnosing

Disclosure; Page 147-49; 305pp; English.

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RESULT 2
AAR34002
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      The sequences given in AAR33992-002 represent a portion of the E2/NS1 protein encoded by group I and group II HCV isolates, from amino acid 370 E2/NS1 are viral envelope proteins and are of immunogenic interest. E2/NS1 contains an N-terminal hypervariable domain of about 30 amino acids which shows large variation between nearly all isolates. This is an important immunoreactive domain. This putative envelope glycoprotein E2/NS1 may correspond to the gpS3(BvDV)/gpS5 (hog cholera virus) envelope polypeptide of the pestiviruses and the NS1 of the flaviviruses, both of which confer protective immunity in hosts vaccinated with these polypeptides. It has been discovered that a number of important HCV epitopes vary among viral isolates and that these epitopes can be mapped to specific domains. This meant that immunologically cross-reactive polypeptides which focus on variable rather than constant domains can be produced. See also AAQ39134-48 and AAR33982-91. (Updated on 25-MAR-2003 to correct PN field.)
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Best Local S
Matches 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Polymerase chain reaction; PCR; amplify; primer; hepatitis C virus; asymptomatic; chronically infected; epitope; viral isolate; domain; immunological; cross-reactive; envelope protein; vaccine; gp53(BVDV)/gp55; hog cholera virus; pestivirus; NS1; flavivirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 alleles of the same region of the HCV gene. Sequence comparisons of these clones showed that it is possible for a patient to carry more than one HCV strain at one time. See also AAQ32436. (Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 283 AA;
                                                                                                                                                                                                                                                                                 Disclosure; Fig 3; 106pp; English.
                                                                                                                                                                                                                                                                                                                  Immuno-reactive hepatitis C virus polypeptide compsns. - contg. at least 2 sequences from the first variable domain of distinct HCV isolates.
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26-JUL-1993
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Pred. No. 9.6e
4; Mismatches
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.6e-29;
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Best Local :
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                                          25-JUN-1990;
31-AUG-1990;
09-NOV-1990;
28-DEC-1990;
08-MAY-1991;
14-MAY-1991;
                                                                                                                                                                                                                                                                          Non-A
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01-MAY-1992
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           WPI; 1992-009412/02.
                        (OSAU )
(REMI-)
                                                                                                                                                                                    Protein
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                                                                                       25-JUN-1991;
                                                                                                   02-JAN-1992
                                                                                                               EP463848-A.
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RES F
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                        V OSAKA.
FOUND MICROBIAL.
                                                                                                                                                                                                                                                                                                                    (revised)
(first entry)
                                           90US-00635451.
91JP-00132090.
91JP-00138493.
                                                              90JP-00167466.
90JP-00230921.
90JP-00305605.
                                                                                       91EP-00305717
                                                                                                                     /label= Ner
                                                                                                                                                                                                                                                                           virus
                                                                                                                                                                1007. .1614
/label= NS3
                                                                                                                                                                                                            192. .389
/label= E
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730. .1006
                                                                                                                                                                                                                  /note= "matrix protein"
192. .389
                                                                                                                                        1863. .2012
/label= NS4b
                                                                                                                                                                                                 390.
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                                                                                                                                                                                                      'note= "envelope
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Pred. No. 1.
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N-PSDB; AAQ20268.

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RESULT 4
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ID AAR20091
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Best Local :
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     EP464287-A
                                                                                                                                                                                       Protein
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01-MAY-1992
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                                                                                                                                     Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    807
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(first entry)
                                                                          1007. .1614
/labelm NS3
/1615. 1862
/labelm NS4a
1863. .2012
/labelm NS4b
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/label= NS2
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85.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                             .389
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 283; DB 2; I
Pred. No. 1.4e-27;
4; Mismatches 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 3010;
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RESULT 5
AAY06423
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The sequence was deduced from several overlapping "BK" cDNA clones obtd. by "gene walking" using a cDNA clone isolated from a library prepd. from NANBV RNA. Antigenic polypeptides from the sequence can be used as immunoassay reagents, for screening donated blood, and as immunogens for vaccine prodn. Antibodies raised to the peptides can be used in immunoassays to detect or quantify NANBV antigens in liver tissue and blood. Preferred polypeptides are include residues 1-30, -115, or 2012; 47-77; 116-191; 192-207 or -298; 230-218 or -263; 287-300; 293-330; 390-729; 730-1005; 1006-1614; 1384-1414; 1615-1862; 1737-1767; 1863-2012; and 2013-3010. The sequence is also disclosed in EP-463848 (SEQ ID NO 1) in which a virus particle conty. antigens encoded by the sequence is claimed. See AAR20111 for details of this specification. (Updated on 25-MAR-2003 to correct PA field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         25-JUN-1990;
31-AUG-1990;
09-NOV-1990;
17-JUN-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 3010 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New DNA from non-A, non-B hepatitis virus - and derived antigenic polypeptide(s) useful for diagnostics, blood screening and in vaccines.
                                                                                                                                                       Non-A,
                                                                                                                                                                                Non-A,
                                                                                                                                                                                                          20-MAR-2003
27-SEP-1999
                                                                                                                                                                                                                                                                           AAY06423 standard; protein; 3010 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           28-DEC-1990;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   08-JAN-1992
            Protein
                                   Protein
                                                              Protein
                                                                                                   non-B hepatitis
                                                                                                                                            vaccine.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1992-009617/02.
                                                                                                                                                                                                                                                                                                                                                                                                  747
                                                                                                                                                                                                                                                                                                                                                                        61
                                                                                                                                                                                                                                                                                                                                                                                                                                                     54;
                                                                                                                                                                                non-B
                                                                                                                                                         non-B
                                                                                                                                                                                                                                                                                                                                                                                                                   1 ALENIVVLNAASAAGTHGILWFLVFFCAAWYVKGRLVPGATYSLLGLWFLLLLLLLALPQR 60
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                                                                                                                                                                                                                                                                                                                                                                      AYA 63
                                                                                                                                                                                                                                                                                                                                                                                               ALENLVVLNSASVAGAHGILSFLVFFCAAWYIKGRLVPGATYALYGVWPLLLLLLALPPR
                                                                                                                                                                                                                                                                                                                                              AYA 809
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2; 89pp;
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                                                                                                                                                       hepatitis B virus; NANBV; antigen; infection; diagnosis;
                                                                                                                                                                                  hepatitis virus polypeptide.
                                                                                                                                                                                                          (revised)
(first entry)
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90JP-00230921
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                                                                                                       virus
                                     116. .191
                                                                         Location/Qualifiers
                       'note= "matrix protein"
                                                 note=
'note= "envelope protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                86.5%;
            .389
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                                                 "core protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                     4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 283; DB 2;
Pred. No. 1.4e-27;
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RESULT 6
ADJ82984
ID ADJ8
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                                                                                                                                                                                                                                                                This sequence represents the non-A, non-B hepatitis virus (NANBV)

[C polypeptide, as predicted from cDNA (see AAX59394) containing the entire open reading frame of the NANBV genome. To obtain this cDNA, NANBV RNAB copen reading frame of the NANBV genome. To obtain this cDNA, NANBV RNAB copen reading frame of the NANBV genome. To obtain this cDNA, NANBV RNAB copen reading frame of the NANBV particles contained in whole blood of a patient having NANB hepatitis, or from a resected liver of a patient double-stranded cDNA. A cDNA library was produced and screened using serum from a convalescent patient having acute NANB hepatitis and serum from a patient having chronic NANB hepatitis. The isolated cDNA allows recombinant production of NANBV antigen polypeptides in microbial or eukaryotic cell culture. The method provides the safe production of NANBV antigens with high purity on a large scale at low cost without the biohazard associated with multiplying virus in animals. Claimed NANBV nucleotide sequences are useful for the recombinant production of polypeptides useful as antigens for vaccines, and as diagnostic reagents. (Updated on 20-MAR-2003 to correct PF field.) (Updated on 20-MAR-2003 to correct PF field.)
                                                                                                                                                                                                     Query Match
Best Local S
Matches 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               25-JUN-1990;
31-AUG-1990;
09-NOV-1990;
28-DEC-1990;
             ADJ82984 standard; protein; 1026 AA.
                                                                                                                                                                                                                                                              Sequence 3010 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 2; Fig 2(1)-(16); 56pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New hepatitis virus polypeptides, useful for diagnosing and treating
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Protein
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                                                                                     807
                                                                                                                                             747
                                                                                                                 61
                                                                                                                                                                                                      54;
                                                                                                                                                           1 ALENLVVLNAASAAGTHGILWFLVFFCAAWYVKGRLVPGATYSLLGLWPLLLLLLALPQR
                                                                                                                                                                                                                                                                                            PR
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                                                                                                                                                                                                                    Similarity
                                                                                     AYA BOS
                                                                                                                  AYA 63
                                                                                                                                               ALENLYVLNSASVAGAHGILSFLVFFCAAWYIKGRLVPGATYALYGVWPLLLLLLALPPR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     infections.
                                                                                                                                                                                                                                                                                            field.)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Fuke I,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               90JP-00167466.
90JP-00230921.
90JP-00305605.
90EP-00314371.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note= "NS2 protein"
1007. .1615
/note= "NS3 protein"
1616. .1862
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       99EP-00106005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      390. .7
/note=
730. .1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note=
2014. .
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/note= "NS4a protein"
1863. .2013
                                                                                                                                                                                                                 86.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .1006
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mori
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "NS4b protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "NS1 protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "NS5 protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ú
                                                                                                                                                                                                   Score 283; DB 2; Length 3010;
Pred. No. 1.4e-27;
4; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Takamizawa
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AAY70064
ID AAY7
XX AAY7
AC AAY7
XC AA
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Best Local Similarity
Matches 54; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present invention relates to a method of producing hepatitis C virus (HCV) particles by incubating Vero cells containing a recombinant nucleic acid that comprises an expression cassette encoding for at least a HCV C-E1-E2-P7-NS2 sequence under conditions suitable for producing the HCV particles. The method is useful for making hepatitis C virus (HCV) particles and measuring the ability of a compound to inhibit HCV particle formation or function. The HCV particles are useful as source materials for obtaining HCV antibodies recognizing a native particle form, and for evaluating the ability of a compound to inhibit particle form, and construct designated HCV C-E1-E2-P7-NS2 used to demonstrate the method of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 1026 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Producing hepatitis C virus (HCV) particles comprises incubating Vero cells containing a recombinant nucleic acid that comprises an expression cassette encoding for at least a HCV C-E1-E2-P7-NS2 sequence.
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N-PSDB; ADJ82983.
                                                                                      Recombinant fusion pHCAP-1 polyprotein.
                                                                                                                                            12-SEP-2003
05-JUN-2000
                                                                                                                                                                                                                                                                                        AAY70064 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; Page 37-39; 53pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO2004005524-A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Adenovector construct HCV C-E1-E2-P7-NS2 protein sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADJ82984;
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                                                                                                                                                                                                                                                                                                                                                                                                                                       807
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                                                                                                                                            (revised)
(first entry)
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                                                                                                                                                                                                                                                                                        protein;
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85.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Graham
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 281; DB 8;
Pred. No. 7.7e-28;
3; Mismatches 6
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Recombinant plasmid; pHCAP; Hepatitis C virus; HCV; reporter gene; NS3 protease; inhibitor; recombinant viral vector; RVV; HCV infection;

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The patent discloses a reporter gene system for use in a cell-based assessment of inhibitors of Hepatitis C virus (HCV) NS3 protease, using a recombinant viral vector (RVV), that expresses a secreted human placental alkaline phosphatase (SEAP) reporter gene polyprotein, under the control of bacteriophage T7 promoter. The viral vector has been engineered to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo
                                                                  Claim 39;
                                                                                      Assessing compounds which augment or inhibit Hepatitis C virus protease, useful particularly for identifying inhibitors which used for treating Hepatitis C virus infections.
                                                                                                                                                                                                            05-AUG-1998;
08-MAR-1999;
                                                                                                                                                                                                                                             02-AUG-1999;
                                                                                                                                                                                                                                                                   17-FEB-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Enterobacteria phage T7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hepatitis C vi:
Vaccinia virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            secreted alkaline phosphatase; SEAP; serine protease; treatment;
recombinant vaccinia virus.
                                                                                                                                                                                       (AGOU-)
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                                                                                                                                 2000-224057/19.
DB; AAZ51002.
                                                                                                                                                                 <u>E</u>
                                                                                                                                                                                       AGOURON PHARM INC.
                                                                 Page 70-78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C virus.
                                                                                                                                                                 Jackson
                                                                                                                                                                                                            98US-00129611.
99US-00263933.
                                                                                                                                                                                                                                            99WO-US017440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /label= NS4A_domain
/note= "Hepatitis C
1076. .1092
                                                                                                                                                                                                                                                                                                                                                                                                                        /label= NS4B_domain
/note= "Hepatitis C
1259 ..1278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HCV/SEAP fragment"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              containing serine protease
                                                                                                                                                                                                                                                                                                                                                                            label= Secreted_alkaline_phosphatase_protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   'label≔ NS4A/NS4B_cleavage site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        label= NS3/NS4A_cleavage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          note= "Hepatitis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        label= E2/NS2_domain
note= "Hepatitis C virus non-structural
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     note= "Additional
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         label pHCAP-1_polyprotein_fragment_2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               label pHCAP-1_polyprotein_fragment_1
                                                                                                                                                                                                                                                                                                                                                                                                               label=
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                                                                                                                                                                                                                                                                                                                                   abel=
                                                                                                                                                                 RL,
                                                                 153pp; English
                                                                                                                                                                                                                                                                                                                                                                                                            NS5A/NS5B_cleavage site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NS3_domain
                                                                                                                                                                 Patick
                                                                                                                                                                                                                                                                                                           pHCAP-1_polyprotein_fragment_5
                                                                                                                                                                                                                                                                                                                                 pHCAP-1_polyprotein_fragment_4
                                                                                                                                                                                                                                                                                                                                                       pHCAP-1_polyprotein_fragment_3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     residues resulting from subcloning
                                                                                                                                                                                                                                                                                                                                                                                                                                     virus non-structural domain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         virus non-structural
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RESULT 8
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          express a polyprotein, that includes NS3 HCV serine protease and the human SEAP gene. This assay system is useful for in vitro screening of potential protease inhibitors useful in the treatment of HCV infections and used to evaluate potent NS3 inhibitors, by monitoring the effect of increasing drug concentration on SEAP activity. NS3 inhibition is decrease in SEAP activity. NS3 inhibition is the recombinant fusion protein, encoded by the RVV pHCAP-1, comprising five segments and the active NS2 and NS3 protease polyproteins, fused with the SEAP reporter protein. The plasmid is constructed using the pTM3 vector and has been used to generate recombinant vaccinia viruses. (Updated on 12-SEP-2003 to standardise OS field)
                                                                                                                                                                                                                                                                                                                                                                                                           Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Key
Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Recombinant plasmid; pHCAP; Hepatitis C virus; HCV; reporter gene; NS3 protease; inhibitor; recombinant viral vector; RVV; HCV infection; secreted alkaline phosphatase; SEAP; serine protease; treatment;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 2307
Cleavage-site
                                                                                                                                                                                  Misc-difference
                                                                                                                                                                                                                                                                                                                                             Domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hepatitis
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05-JUN-2000
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                                                                     Domain
                                                                                                             Cleavage-site
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(first entry)
                                                                                                                                                                                                   /label= NS3_domain
/note= "Hepatitis C virus non-structural
containing serine protease and helicase o
                                                                                                                                                                                                                                                                                                                                                                /note= "Additional
HCV/SEAP fragment"
                                                                                                                                     inactivate NS3
                                                                                                                                                                                                                                                                                                                                                                                                                                                          ocation/Qualifiers
                     label= NS4A_domain
note= "Hepatitis C
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                                                                                                                                                             note= "Wild
                                                                                                                                                                                                                                                                                             label= E2/NS2_domain
note= "Hepatitis C v:
                                                                                                                                                                                                                                                                                                                                                                                                                                  label= pHCAP-1_polyprotein_fragment_2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            protein; 2307
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                                                                  .1082
                                                                                          NS3/NS4A_cleavage
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                                                                                                                                  type catalytic
33 protease"
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Pred. No. 1.9e-27;
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                       non-structural
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                            domain"
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RESULT 9
AAY70066
                                                                                                                                                                                                                                                                                                                                                                                                        The patent discloses a reporter gene system for use in a cell-based cassessment of inhibitors of Hepatitis C virus (HCV) NS3 protease, using a recombinant viral vector (RVV), that expresses a secreted human placental classes and phosphatase (SBAP) reporter gene polyprotein, under the control of bacteriophage T7 promoter. The viral vector has been engineered to express a polyprotein, that includes NS3 HCV serine protease and the human SEAP gene. This assay system is useful for in vitro screening of potential protease inhibitors useful in the treatment of HCV infections and used to evaluate potent NS3 inhibitors, by monitoring the effect of increasing drug concentration on SEAP activity. NS3 inhibition is detected as a decrease in SEAP activity. The present sequence is the recombinant fusion protein, encoded by the RVV pHCAP-3, comprising five segments and the active NS2 and mutant NS3 protease, fused with the SEAP reporter protein. The NS3 protease is inactivated by site directed mutagenesis. The plasmid is constructed using the pTM3 vector and has been used to generate recombinant vaccinia viruses. (Updated on 12-SEP-C 2003 to standardise OS field)
                                                                                                                                                                                                                                                                          Query Match
Best Local S
Matches 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Assessing compounds which augment or inhibit Hepatitis C virus protease, useful particularly for identifying inhibitors which used for treating Hepatitis C virus infections.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Domain
                                                                                                                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                05-AUG-1998;
08-MAR-1999;
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                                                                                                                                                                                                                                                                            Conservative
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99US-00263933.
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/note= "Secreted human placental SEAP"
1785 . 1936
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/note= "Hepatitis C virus non-structural domain"
/1259. .1278
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1083. .1257
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                                                                                                                                                                                                                                                                                               85.9%;
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    .2021
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                                                                                                                                                                                                                                                                          Score 281; DB 3;
Pred. No. 1.9e-27;
3; Mismatches 6;
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(AGOU-) AGOURON PHARM INC

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Region
                   05-AUG-1998;
08-MAR-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hepatitis C virus. Vaccinia virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Recombinant plasmid; pHCAP; Hepatitis C virus; HCV; reporter gene; NS3 protease; inhibitor; recombinant viral vector; RVV; HCV infection; secreted alkaline phosphatase; SEAP; serine protease; treatment;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          12-SEP-2003
05-JUN-2000
                                                   02-AUG-1999;
                                                                        17-FEB-2000.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 recombinant vaccinia virus.
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(first entry)
                   98US-00129611.
99US-00263933.
                                                   99WO-US017440
                                                                                                                                                                                                                                                                            1019. .1038
/label= NS3/NS4A_cleavage site
1029. .1082
/label= NS4A_domain
/note= "HepaTitis C virus non-structural
1076. .1092
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note= "Additional residues resulting from subcloning
HCV/SEAP fragment"
                                                                                                                                                                                                                                                                                                                                                                           /label= NS3_domain
/note= "Hepatitis C virus non-structural domain
containing serine protease and helicase enzymes"
                                                                                                                                                                                                                        /label= NS4B_domain
/note= "Hepatitis C virus non-structural domain"
1259. .1278
                                                                                                                                                                                                                                                       /label= NS4A/NS4B_cleavage site
1083. .1257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
                                                                                                                                                                    label= Secreted alkaline phosphatase protein note= "Secreted human placental SEAP" 785. 1936
                                                                                                                                                                                                                                                                                                                                           nactivate NS3 protease"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          label= pHCAP-1_polyprotein_fragment_2
\3. .98
                                                                                                                                                                                                             label= NS5A/NS5B_cleavage site
                                                                                                                                                                                                                                                                                                                                                       note= "Wild type catalytic Ser replaced with Ala,
                                                                                                                                                                                                                                                                                                                                                                                                                      note= "Wild type catalytic Cys replaced with Ala, nactivate NS2 protease"
                                                                                                                                                                                                                                                                                                                                                                                                                                                     label= E2/NS2 domain
note= "Hepatifis C virus non-structural domain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        label= pHCAP-1_polyprotein_fragment_1
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                                                                                                                                                                                                                                                                                                                                                                                                                    nactivate NS2
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                                                                                                                            l= pHCAP-1_polyprotein_fragment_4
.2307
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                                                                                                                                                          pHCAP-1_polyprotein_fragment_3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CC The patent discloses a reporter gene system for use in a cell-based CC assessment of inhibitors of Hepatitis C virus (HCV) NS3 protease, using a CC recombinant viral vector (RVV), that expresses a secreted human placental CC alkaline phosphatase (SEAP) reporter gene polyprotein, under the control CC of bacteriophage T7 promoter. The viral vector has been engineered to CC express a polyprotein, that includes NS3 HCV serine protease and the CC human SEAP gene. This assay system is useful for in vitro screening of CC potential protease inhibitors useful in the treatment of HCV infections and used to evaluate potent NS3 inhibitors, by monitoring the effect of CC increasing drug concentration on SEAP activity. NS3 inhibition is CC increasing drug concentration on SEAP activity. NS3 inhibition is CC esegments and the mutant inactive NS2 and mutant sequence is the CC recombinant fusion protein, encoded by the RVV pHCAP-4, comprising five CC segments and the mutant inactive NS2 and mutant inactive NS3 protease polyproteins, fused with the SEAP reporter protein. The NS2-NS3 domains CC using the pTM3 vector and has been used to generate recombinant vaccinia CC viruses. (Updated on 12-SEP-2003 to standardise OS field)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                       HCV; Con 1; adaptive mutation; liver failure; cirrhosis; mutant; mutein; hepatocellular carcinoma; NS3; NS5; encephalomyocarditis virus; EMCV; internal ribosome entry site; IRES; NS5A; HCV replication; polyprotein.
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23-JAN-2001; 2001US-0263479P.
                                                         16-JAN-2002; 2002WO-EP000526
                                                                                                                                                                                                                                                                             Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hepatitis C
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                                                                                                                                                                                   WO200259321-A2
                                                                                                                                                                                                                                                                                                                                                                                                    Hepatitis C virus.
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                                                                                                                                                                                                                                                                       Location/Qualifiers
                                                                                                                                                                                                                                          note= "Wild-type Phe substituted by
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RESULT 11 ABG32459

ABG32459 standard; protein; 3010 AA

HCV; Con 1; adaptive mutation; liver failure; cirrhosis; mutant; mutein; hepatocellular carcinoma; NS3; NS5; encephalomyocarditis virus; EMCV; internal ribosome entry site; IRES; NSSA; HCV replication; polyprotein.

Hepatitis C virus Con 1 isolate polyprotein mutant #8.

(first entry)

ney Misc-difference 2198

Hepatitis C virus

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1 ALENLVVLNAASAAGTHGILWFLVFFCAAWYVKGRLVPGATYSLLGLWPLLLLLLALPQR 60

Best Loc Matches Query Match

54;

Conservative

Local

Similarity

85.9%;

Score 281; DB 5; Pred. No. 2.6e-27; Mismatches

Length 3010; Indels

9

0,

Gaps

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CC vector comprising a nucleotide sequence coding for the altered nucleic CC acids, which is transcriptionally coupled to an exogenous promoter; (2) a CC recombinant cell human hepatoma cell comprising the altered nucleic acids (3) a recombinant cell produced by introducing into a human hepatoma (cell the altered nucleic acids; (4) producing into a human hepatoma (cell the altered nucleic acids; (4) producing into a human hepatoma (cell the altered nucleic acids; (4) producing an HCV (hepatitis C virus) (con enhanced cells made in the method; and (6) measuring the continuous cells are useful in studying HCV replicons and HCV replicon enhanced cells are useful in studying HCV replicons and HCV creplicon and HCV creplicon and HCV creplicon and HCV creplicon and HCV and host cell interactions, producing HCV RNA and CC proteins, and providing a system for measuring the ability of a compound CC to modulate one or more HCV activities e.g. to discover drugs which may CC treat HCV mediated diseases such as liver failure, cirrhosts and CC hepatocellular carcinoma. The present sequence is the HCV replicon Con 1 CC polyprotein (comprising the Core, E1, E2, P7, N32, N34A, N34B, N35A mutant of the invention. Note: The present con 1 consist the HCV sequence appearing as ABG32451 and the information in claim consists the HCV sequence appearing as ABG32451 and the information in claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NRS3 or HCV NRS5 encoding region, or encephalomyocarditis virus (EMCV) internal ribosome entry site (IRES) region coding for one or more NRS3, NRS5A, or EMCV IRES mutations, respectively. The location of the mutations are detailed in the specification. Also included are (1) an expression
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Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 1; Page; 69pp; English
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  3010 AA;
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RESULT 12
ABG32451
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to nucleic acid molecules comprising altered HCV CC NS3 or HCV NS5 encoding region, or encephalomyocarditis virus (EMCV) CC NS5A, or EMCV IRES mutations, respectively. The location of the mutations CC are detailed in the specification. Also included are (1) an expression CC vector comprising a nucleotide sequence coding for one or more NS3, CC acids, which is transcriptionally coupled to an exogenous promoter; (2) a recombinant cell human hepatoma cell comprising the altered nucleic acids; (3) a recombinant cell produced by introducing into a human hepatoma CC; (3) a recombinant cell produced by introducing into a human hepatoma CC replicon enhanced cell or which containing a functional HCV replicon; (5) CC an HCV replicon enhanced cells are useful in studying HCV replicons and HCV ceplicon enhanced cells are useful in studying HCV replicons and HCV ceplicon enhanced cells are useful in studying HCV replication and HCV cells are useful in studying HCV replication and CC expression, and HCV and host cell interactions, producing HCV RNA and CC expression, and providing a system for measuring the ability of a compound to more HCV activities e.g. to discover drugs which may treat HCV mediated diseases such as liver failure, cirrhosis and CC hepatocellular carcinoma. The present sequence is the HCV replicon COn 1 polyprotein (comprising the Core, El, E2, P7, NS2, NS3, NS4A, NS4B, NS5A and CC and NS5B proteins), NS5A mutant of the invention. Note: The present present sequence is not shown in the specification but was created by the indexer using the HCV sequence appearing as ABG32451 and the information in claim
                                                                                                                                                                                                                                                                                                                                                                           Matches
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Best Local &
               Hepatitis C virus Con 1 isolate polyprotein
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                                                    15-NOV-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 3010 AA;
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                                                                                                                          ABG32451 standard; protein; 3010
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                                                                                                                                                                                                                                                                                                 Similarity
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                                                    (first entry)
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; Pred. No. 2.6e
3; Mismatches
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.6e-27;
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The invention relates to nucleic acid molecules comprising altered HCV CC NS3 or HCV NS5 encoding region, or encephalomyocarditis virus (EMCV) CC internal ribosome entry site (IRES) region coding for one or more NS3, CC NS5A, or EMCV IRES mutations, respectively. The location of the mutations cere detailed in the specification. Also included are (1) an expression convector comprising a nucleotide sequence coding for the altered nucleic acids, which is transcriptionally coupled to an exogenous promoter; (2) a recombinant cell human hepatoma cell comprising the altered nucleic acids (3) a recombinant cell produced by introducing into a human hepatoma cell the altered nucleic acids; (4) producing an HCV (hepatitis C virus) creplicon enhanced cells made in the method; and (6) measuring the ability of a compound to affect HCV activity. The HCV replicons and HCV replicon enhanced cells made in the method; and (6) measuring the expression, and HCV and host cell interactions, producing HCV RNA and CC replicon enhanced cells are useful in studying HCV replication and CC expression, and HCV and host cell interactions, producing HCV RNA and CC enterins, and providing a system for measuring the ability of a compound compound contents. The present sequence is the HCV replicon Con 1 contents and compound contents and contents
Sequence 3010
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 1; Page 34-36; 69pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      expression.
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ДĀ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Migliaccio G,
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RESULT 13
ABG32455
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Best Local (
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15-NOV-2002
                           ABG32455;
                                                   ABG32455
                                                                                                                                                                                                                                      Local Similarity
                                                                                                                                                                      747 ALENLYVLNAASVAGAHGILSFLVFFCAAWYIKGRLVPGAAYALYGVWPLLLLLLALPPR 806
                                                                                                                                             61
                                                                                                                                                                                                                          54;
                                                                                                                                                                                      1 ALENLYVLNAASAAGTHGILWFLVFFCAAWYYKGRLVPGATYSLLGLWPLLLLLLALPQR 60
                                                                                                                                             AYA 63
                                                  standard; protein; 3010
                                                                                                                   AYA 809
                                                                                                                                                                                                                          Conservative
 (first entry)
                                                                                                                                                                                                                                      85.9%;
85.7%;
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                                                                                                                                                                                                                          Score 281; DB 5;
Pred. No. 2.6e-27;
3; Mismatches 6
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Hepatitis C virus Con 1 isolate polyprotein mutant #4.

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CC Internal ribosome entry site (IRES) region coding for one or more NS3, CC NS3 or HCV NS5 encoding region, or encephalomyocarditis virus (EMCV)
CC internal ribosome entry site (IRES) region coding for one or more NS3, CC NS5A, or EMCV IRES mutations, respectively. The location of the mutations are detailed in the specification. Also included are (1) an expression cc are detailed in the specification. Also included are (1) an expression excise, which is transcriptionally coupled to an exogenous promoter; (2) a recombinant cell produced by introducing into a human hepatoma cell comprising the altered nucleic acids; (4) producing an HCV (hepatitis C virus) cc [1] the altered nucleic acids; (4) producing an HCV (replicon; (5) an HCV replicon enhanced cells made in the method; and (6) measuring the ability of a compound to affect HCV activity. The HCV replicons and HCV replicon enhanced cells are useful in studying HCV replication and ECC expression, and HCV and host cell interactions, producing HCV RNA and CC produlate one or more HCV activities e.g. to discover drugs which may creat HCV mediated diseases such as liver failure, cirrhosis and CC polyproteins (comprising the present sequence is the HCV replicon Con 1 conjuncted in the specification but was created by the indexer using the HCV sequence appearing as ABG32451 and the information in claim creation the specification but was created by the indexer using the HCV sequence appearing as ABG32451 and the information in claim
                                                                                                                                                                                                                                                                                                             Query Match
Best Local 9
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                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 3010 AA;
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NS3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New Hepatitis C virus (HCV) replicons comprising altered HCV NS3 or HCV NS5 encoding region, or encephalomyocarditis virus (EMCV) internal ribosome entry site (IRES) region, useful in studying HCV replication and
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807
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                                                                                                                                                                                                                                                                                                         85.9%;
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Pred. No. 2.6e-27;
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Query Match Best Local Similarity

85.9**%**;

Score 281; DB 5; Pred. No. 2.6e-27;

Length 3010;

Sequence 3010

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RESULT 14
ABG32457
CC vector comprising a nucleotide sequence coding for the altered nucleic CC acids, which is transcriptionally coupled to an exogenous promoter; (2) a CC recombinant cell human hepatoma cell comprising the altered nucleic acids CC; (3) a recombinant cell produced by introducing into a human hepatoma CC replicon enhanced cell or which containing a functional HCV replicon; (5) CC replicon enhanced cells made in the method; and (6) measuring the CC ability of a compound to affect HCV activity. The HCV replicons and HCV replicon enhanced cells made in the method; and (6) measuring the CC replicon enhanced cells are useful in studying HCV replicons and HCV creplicon and HCV creplicon enhanced cells are useful in studying HCV replicons and HCV creplicon and CC comprision, and providing a system for measuring the ability of a compound CC condulate one or more HCV activities e.g. to discover drugs which may CC treat HCV mediated diseases such as liver failure, citrhosts and CC hepatocellular carcinoma. The present sequence is the HCV replicon Con 1 polyprotein (comprising the Core, E1, E2, P7, N32, N34A, N34B, NS5A mutant of the invention. Note: The present sequence is not shown in the specification but was created by the indexer using the HCV sequence appearing as ABG32451 and the information in claim
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to nucleic acid molecules comprising altered HCV NS3 or HCV NS5 encoding region, or encephalomyocarditis virus (EMCV) internal ribosome entry site (IRES) region coding for one or more NS3, NS5A, or EMCV IRES mutations, respectively. The location of the mutations are detailed in the specification. Also included are (1) an expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New Hepatitis C virus (HCV) replicons comprising altered HCV NS3 or HCV NS5 encoding region, or encephalomyocarditis virus (EMCV) internal ribosome entry site (IRES) region, useful in studying HCV replication and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 1; Page; 69pp; English.
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The invention relates to nucleic acid molecules comprising altered HCV CR NS3 or HCV NS5 encoding region, or encephalomyocarditis virus (EMCV) CC internal ribosome entry site (IRES) region coding for one or more NS3, CC NS5A, or EMCV IRES mutations, respectively. The location of the mutations created in the specification. Also included are (1) an expression cc vector comprising a nucleotide sequence coding for the altered nucleic acids, which is transcriptionally coupled to an exogenous promoter; (2) a recombinant cell human hepatoma cell comprising the altered nucleic acids (3) a recombinant cell produced by introducing into a human hepatoma cell the altered nucleic acids; (4) producing an HCV (hepatitis C virus) Creplicon enhanced cells made in the method; and (5) measuring the cability of a compound to affect HCV activity. The HCV replicons and HCV replicon enhanced cells made in the method; and (6) measuring the contains, and providing a system for measuring the ability of a compound contains, and providing a system for measuring the ability of a compound conducted the contains, producing HCV RNA and contains, and providing a system for measuring the ability of a compound conducted one or more HCV activities e.g. to discover drugs which may treat HCV mediated diseases such as liver failure, cirrhosis and conjugation con 1 properties of the HCV replicon c
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Search completed: October 4, 2005, 18:56:23 Job time : 168 secs

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2: /cgn2 6/ptodata/1
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Listing first 45 summaries
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GenCore version 5.1.6 (c) 1993 - 2005 Compugen Ltd
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       US-09-263-933-23
US-09-919-901-23
US-10-191-966-23
US-08-324-977-38
US-08-315-850-38
US-08-315-850-38
US-08-315-850-38
US-08-315-850-38
US-08-315-850-32
US-08-324-977-12
US-08-324-977-32
US-08-324-977-32
US-08-324-977-36
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Result

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Sequence 2, Appl	Sequence 16, App	Sequence 9, Appl	Sequence 2, Appl	Sequence 18, App	Sequence 11, App	Sequence 4, Appl	Sequence 18, App	Sequence 11, App.	Sequence 4, Appl:	Sequence 18, App	Sequence 11, App.	Sequence 4, Appl	Sequence 14, App	Sequence 2, Appl	Sequence 14, App	Sequence 2, Appl:	Sequence 14, App
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ALIGNMENTS

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CURRENT APPLICATION NUMBER: US/09/263,933
CURRENT FILING DATE: 1999-03-08
EBARLIER APPLICATION UNMBER: 09/129,611
EARLIER FILING DATE: 1998-08-05
NUMBER OF SEQ ID NOS: 33
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 23
LENGTH: 88
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
                         RESULT 2
US-09-919-901-23
; Sequence 23, Application US/09919901
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APPLICANT: Potts, Karen E.
APPLICANT: Jackson, Roberta L.
APPLICANT: Jackson, Roberta L.
APPLICANT: Patick, Amy K.
APPLICANT: Patick, Amy K.
APPLICANT: PATICH, Amy K.
APPLICANT: PATICH, FAMILY AMDERING SYSTEM FOR USE IN CELL-BASED ASSESSMENT TITLE OF INVENTION: OF INHIBITORS OF THE HEPATITIS C VIRUS PROTEASE FILE REFERENCE: 0125-0005A
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Best Local Similarity
Matches 54; Conserv
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Patent No. 628094
FILE REFERENCE: 0125-0005A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OTHER INFORMATION: OTHER INFORMATION:
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milarity 85.7%;
Conservative
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Pred. No. 6.2e-29;
4; Mismatches 5;
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US-08-324-977-38
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PRIOR FILING DATE: 1998-08-05
NUMBER OF SEQ ID NOS: 33
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 23
                                                                                                                                                                                                                                                                                                                                               SEQ ID NO 23
LENGTH: 88
TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                          Query Match
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: BOTTS, Karen E.
APPLICANT: Jackson, Roberta L.
APPLICANT: Jackson, Roberta L.
APPLICANT: Jackson, Roberta L.
APPLICANT: Patick, Amy K.
TITLE OF INVENTION: REPORTER GENE SYSTEM FOR USE IN CELL-BASED ASSESSMENT
TITLE OF INVENTION: OF INHIBITORS OF THE HEPATITIS C VIRUS PROTEASE
FILE REFERENCE: 0125-0005A
CURRENT APPLICATION NUMBER: US/10/191,966
CURRENT FILING DATE: 2002-07-10
PRIOR APPLICATION NUMBER: US/09/263,933
PRIOR TILING DATE: 1999-03-08
PRIOR APPLICATION NUMBER: 09/129,611
PRIOR APPLICATION NUMBER: 09/129,611
PRIOR FILING DATE: 1998-08-05
RUMBER OF SEQ ID NOS: 33
CONTRADED TO NOS: 33
CONTRADED TO NOS: 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -09-919-901-23
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CURRENT FILING DATE: 2001-08-02
PRIOR APPLICATION NUMBER: 09/263,933
PRIOR FILING DATE: 1999-02-08
                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: PatentIn Ver. 2.0
                                                                                                                                                                                                                                                                                          FEATURE: OTHER INFORMATION: Description of Artificial Sequence: amino acid OTHER INFORMATION: fragment of the HCV polyprotein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Artificial Sequence .
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: amino acid
OTHER INFORMATION: fragment of the HCV polyprotein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 88
TYPE: PRT
                                                                                                                                                                                                                          Local Similarity
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5, 6790612
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                                                                                                                                    ALENLVVLNAASAAGTHGILWFLVFFCAAWYVKGRLVPGATYSLLGLWPLLLLLLALPQR 60
                                                                                                    AYA 63
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                                                                     AYA 81
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Pred. No. 6.2e-29;
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Pred. No. 6.2e-29;
4; Mismatches 5;
                                                                                                                                                                                                                                       Length 88;
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Sequence 38, Application US/08324977
Patent No. 5747339
GENERAL INFORMATION:
APPLICANT: OXAYAMA, Hiroto
APPLICANT: FUXE, Isao
APPLICANT: TAXAMIZAWA, Akahisa
APPLICANT: YOSHIDA, Iwao
                                                                                                                                                                                                                                  ; TOPOLOGY: linear; MOLECULE TYPE: protein US-08-324-977-38
                                                                                                                                                     Query Match
Best Local S
Matches 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE: 31-AUG-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 2-305605
FILING DATE: 09-NOV-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/099,706
FILING DATE: 30-JUL-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/769,996
ETILING DATE: 02-OCT-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/635,451
FILING DATE: 28-DEC-1990
                                                                                                                                                                                                                                                                                                                                   TELEX: 440142
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/08/
FILING DATE: 18-OCT-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 2-1
FILING DATE: 25-UTN-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 2-2
APPLICATION NUMBER: JP 2-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE: Diskette, 3.5 in, 1.44Mb
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS, Version 5.0
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY: U.S.A.
ZIP: 20006
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: YOSHIDA, IWAO
TITLE OF INVENTION: NON-A, NON-B HEPATITIS VIRUS GENOMIC
TITLE OF INVENTION: CDNA AND ANTIGEN POLYPEPTIDE
                                                                                                                                                                                                                                                                                                                                                                                                                    TELECOMMUNICATION INFORMATION: TELEPHONE: (202) 659-2930
                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
NAME: Stevens-Smith, Theres
REGISTRATION NUMBER: 36,281
REFERENCE/DOCKET NUMBER: 90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STREET: 1725 K Strate: Washington STATE: D.C.
                                                                                                                                                                                                                                                                                                                                                                                   TELEPHONE: (202) 887-0357
                                                                                                                                                                            Local Similarity
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                                                                                                                                                                                                                                                                                                                LENGTH: 277 amino acids
78
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                                   61 AYA 63
                                                                                                                                                         54;
                                                                                             1 ALENLVVLNAASAAGTHGILWFLVFFCAAWYVKGRLVPGATYSLLGLWPLLLLLLLALPQR 60
                                                                                                                                                                                                                                                                                            amino acid
                                                                          ALENLYVLNSASVAGAHGILSFLVFFCAAWYIKGRLVPGATYALYGVWPLLLLLLALPPR
AYA 80
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                                                                                                                                                         Conservative
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                                                                                                                                                                          86.5%;
85.7%;
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                                                                                                                                                         4.
                                                                                                                                                     Score 283; DB 1;
Pred. No. 2.4e-28;
4; Mismatches 5
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                                                                                                                                     Matches
                                                                                                                                                   Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PILING DATE:

CLASSIFICATION: 424

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/769,996

APPLICATION NUMBER: US 07/769,996

FILING DATE: 02-0CT-1991

APPLICATION NUMBER: UP 2-167466

FILING DATE: 25-UN-1990

PRIOR APPLICATION DATA:

APPLICATION NUMBER: UP 2-30921

FILING DATE: 31-AUG-1990

PRIOR APPLICATION DATA:

APPLICATION NUMBER: UP 2-305605

FILING DATE: 09-NOV-1990

PRIOR APPLICATION DATA:

APPLICATION DATA:

APPLICATION DATA:

APPLICATION DATA:
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INFORMATION FOR SEQ ID NO: 38:
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/384,616
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT:
                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
LENGTH: 277 amino acide
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MEDIUM TYPE: Diskette, 3.5 in, 1.44Mb
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS, Vers:
                                                                                                                                                                                                                                                                                                                                                          TELECOMMUNICATION INFORMATION: TELEPHONE: (202) 659-2930
                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US 07/635,451 FILING DATE: 28-DEC-1990 ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: NON-A, NON-B HEPATITIS VIRUS
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CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                        NAME: Stevens-Smith, Theres REGISTRATION NUMBER: 36,281 REFERENCE/DOCKET NUMBER: 90
                                                                                                                                                                                                                                    TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                           TELEFAX:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: Armstrong, Westerman, Hattori, McLeland
                                                                   18
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78
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                                 AYA 63
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AYA 80
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1725 K St. N.W. Suite 1000
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Chisato
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                                                                                                                                     Conservative
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                                                                                                                                                   86.5%;
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                                                                                                                                 Score 283; DB 2; Length 27
Pred. No. 2.4e-28;
4; Mismatches 5; Indels
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                                                                                                                                                                 Length 277;
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                                                Matches
                                                                 Best Local Similarity
                                                                                 Query Match
                                                                                                                                                                                                                                 TELEFAX: (202) 887-03
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE: 31-AUG-1S
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 31
APPLICATION NUMBER: 09-NOV-11
FILING DATE: 09-NOV-11
FRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ZIP: 20006
COMPUTER READABLE FORM:
MEDIUM TYPE: Disketto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/08/904,686A FILING DATE: 01-AUG-1997 PRIOR APPLICATION DATA: APPLICATION NUMBER: US 08/324,977 FILING DATE: 18-OCT-1994 PRIOR APPLICATION NUMBER: US 08/324/977 PRIOR APPLICATION NUMBER: US 08/324/977 PRIOR APPLICATION NUMBER: US 0-167466
                                                                                                                                                                                                                                                                      NAME: McLeland, Le-Nhung
REGISTRATION NUMBER: 31,541
REFERENCE/DOCKET NUMBER: 90
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 659-2930
                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: JP 2-
FILING DATE: 25-JUN-1990
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS, Version 5.0
SOUTWARE ASCII
CURRENT APPLICATION DATA:
                                                                                                                                       MOLECULE TYPE: protein
                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: 1
FILING DATE: 30-JUL-
PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: NON-A, NON-B HEPATITIS VIRUS GENOMIC TITLE OF INVENTION: CDNA AND ANTIGEN POLYPEPTIDE
                                                                                                                                                                                                                                                                                                                                                                 FILING DATE: 28-DEC-1990 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STREET: 1725 K STREET: Washington
                                                                                                                                                            TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: Naughton
STREET: 1725 K St. N.W. Suite 1000
                                                                                                                                                                                               ENGTH:
1 ALENLVVLNAASAAGTHGILWFLVFFCAAWYVKGRLVPGATYSLLGLWPLLLLLLLALPQR
                                                                                                                                                                       : 277 amino acids amino acid
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                                                Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Diskette, 3.5 in, 1.44Mb
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                                                               86.5%;
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                                              Score 283; DB 2; Length 277; Pred. No. 2.4e-28; 4; Mismatches 5; Indels
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ALENLYVLNSAS VAGAHGILSFLVFFCAAWYIKGRLVPGATYALYGVWPLLLLLLALPPR 77

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GENERAL INFORMATION:
                                                                                                               TELEPHONE: (202) 659-2930
TELEFAX: (202) 887-0357
INFORMATION FOR SEQ ID NO: 38
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MOLECULE TYPE: protein
)-315-850-38
                                                                                                                                                                   NAME: MCLeland, Le-Nhung
REGISTRATION NUMBER: 31,541
REFERENCE/DOCKET NUMBER: 900703G
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/635,451
FILING DATE: 28-DEC-1990
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE: 25-JUN-1990
PRIOR APPLICATION UMATA:
APPLICATION UMBER: JP 2-230921
FILING DATE: 31-AUG-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/904,686
FILING DATE: 01-AUG-1997
APPLICATION NUMBER: US 08/324,977
FILING DATE: 18-OCT-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE: Diskette, 3.5 in, 1.44Mb COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS, Version 5.0 SOFTWARE: ASCII CURRENT APPLICATION DATA: APPLICATION NUMBER: US/09/315,850
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APPLICATION NUMBER: JP 2-167466
                                                                                           SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 2-
FILING DATE: 09-NOV-1990
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CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: NON-A, NON-B HEPATITIS VIRUS
                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
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                    TYPE: amino acids
TYPE: amino acid
TOPOLOGY: lines-
LECUIT
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                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE: 30-JUL-1993
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1725 K St. N.W. Suite 1000
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MORI, Chisato
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FILING DATE:
APPLICATION NUMBER: US 07/759,575
FILING DATE: 13-SEP-1991
ATTORNEY/AGENT INFORMATION:
NAME: MCCLUNG, Batbara G.
REGISTRATION NUMBER: 33,113
REGISTRATION NUMBER: 0205.001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (510) 601-2708
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
Matches 54; Conserv
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                                                                                                              Matches
                                                                                                                          Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIA RELEASE #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/440,103
FILING DATE: 12-MAY-1995
CLASSIFICATION: 424
CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ZIP: 94608
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
LENGTH: 480 amino acids
TYPE: amino acid
STRANDEDNESS: single
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Chiron Co
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Weiner, Amy J.
APPLICANT: Houghton, Michael
TITLE OF INVENTION: Immunoreactive Polypeptide Compositions
                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
APPLICATION NUMBER:
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AYA 440
                          AYA 63
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ilarity 85.7%;
Conservative
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Pred. No. 2.4e-28; 
4; Mismatches 5; Indels
                                                                                                           Score 283; DB 1; Pred. No. 4.6e-28; 4; Mismatches 5;
                                                                                                                                      Length 480;
                                                                                                              Indels
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Best Local S
Matches 54
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                                                                                                                                                                               Sequence 22, Application US/08231368
Patent No. 5756312
GENERAL INFORMATION:
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INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US/08/440,542
PILING DATE: 12-MAY-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/231,368
FILING DATE:
APPLICATION NUMBER: US 07/759,575
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE: 13-SEP-1991
ATTORNEY/AGENT INFORMATION:
NAME: McClung, Barbara G.
REGISTRATION NUMBER: 33,113
REFERENCE/DOCKET NUMBER: 0205.001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (510) 601-2708
                                                                                    APPLICANT: Weiner, Amy J.
APPLICANT: Houghton, Michael
TITLE OF INVENTION: Immunoreactive Polypeptide Compositions
NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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APPLICANT: Houghton, Michael
TITLE OF INVENTION: Immunoreactive Polypeptide Compositions
NUMBER OF SEQUENCES: 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 480 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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                               CITY: Emeryville
                                                    STREET:
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COUNTRY:
                                                                      ADDRESSEE:
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No. 5670153
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                                                                                                                                                                                                                                                                                                                                                     61 AYA 63
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                                                    4560 Horton Street
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                                                                      Chiron Corporation
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85.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 283; DB 1; L
Pred. No. 4.6e-28;
4; Mismatches 5;
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US-08-440-210-22
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                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 22, Application US/08440210 Patent No. 5766845
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
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                                                                                                                                                                                                                                                                                                                                       ATERT NO. 37.00.10N:
GENERAL INFORMATION:
APPLICANT: Heiner, Amy J.
APPLICANT: Houghton, Michael
APPLICANT: Houghton, Immunoreactive Polypeptide Compositions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity
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INFORMATION FOR SEQ ID NO: 3
SEQUENCE CHARACTERISTICS:
LENGTH: 480 amino acids
                              FILING DATE: 12-MAY-19
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION UNMBER: US
FILING DATE:
                                                                                                MEDIUM TYPE: Floppy disk
COMPUTER: IRM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARB: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION UMBER: US/08/440,210
FILING DATE: 12-MAY-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
NAME: McClung, Barbara G.
REGISTRATION NUMBER: 33,113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 0
FILING DATE: 13-SEP-1991
                                                                                                                                                                                                      COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER: 02
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                  STREET: 4560 nor.
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ZIP: 94608
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TOPOLOGY: linear
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APPLICATION NUMBER: US 07/759,575 FILING DATE: 13-SEP-1991
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 AYA 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            54;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 ALENLYVINAASAAGTHGILWFLVFFCAAWYVKGRLVPGATYSLLGLWPLLLLLLALPQR
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                                                                                                                                                                                                                                                                                                           E: Chiron Corporation
4560 Horton Street
                                                                                                                                                                                                                                                        USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (510) 655-3542
(510) 10 NO: 22:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (510) 601-2708
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                                                   US/08/231,368
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 283; DB 1; Length 480; Pred. No. 4.6e-28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0205.001
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TOPOLOGY: 1:

; MOLECULE TYPE:

US-09-046-604-22
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELECOMMUNICATION INFORMATION: TELEPHONE: (510) 601-2708
TELEPAX: (510) 655-3542
INFORMATION FOR SEQ ID NO: 22:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
APPLICANT: Weiner, Amy J.
APPLICANT: Houghton, Michael
TITLE OF INVENTION: Immunoreactive Polypeptide Compositions
NUMBER OF SEQUENCES: 45
                                                                                                                   TELEFAX: (510) 655-3542
NFORMATION FOR SEQ ID NO: 22:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       quence 22, Application US/09046604
tent No. 6303292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
LENGTH: 480 amino acid
                                                                                                SEQUENCE CHARACTERISTICS:
                                                                                                                                                                  NAME: McClung, Barbara G.
REGISTRATION NUMBER: 33,13
REFERENCE/DOCKET NUMBER: 0205.001
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                    FILING DATE:
APPLICATION NUMBER: US 07/759,575
FILING DATE: 13-SEP-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION DATA: APPLICATION NUMBER: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
ADDRESSEE: Chiron Corporation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: protein
                                         LENGTH: 480 amino
TYPE: amino acid
STRANDEDNESS: sin
                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                          MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 480 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: McClung, Barbara G. REGISTRATION NUMBER: 33,1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REGISTRATION NUMBER: 33,113
REFERENCE/DOCKET NUMBER: 0205.001
                                                                                                                                                    TELEPHONE:
                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 AYA 63
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     S
                                                                              480 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4560 Horton Street
                          linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                     (510) 601-2708
            protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               86.5%;
                                                                                                                                                                                                                                                                                                         US/08/231,368
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Pred. No. 4.6e-28;
4; Mismatches 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 480;
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RESULT 13
US-08-324-977-12
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Best Local Similarity 85.7
Matches 54; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
APPLICANT: OKAYAMA
APPLICANT: FUKE, I
APPLICANT: MORI, C
APPLICANT: TAKAMIZ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 12, Application US/08324977 Patent No. 5747339
                                                                                                                                                                                                                                                                                                                                                                                                                                           OPERTING SYSTEM: PC-DOS/MS-DOS, Ve. SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/324,977
FILING DATE: 18-OCT-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 2-167466
FILING DATE: 25-JUN-1990
PRIOR APPLICATION NUMBER: JP 2-230921
FILING DATE: 31-AUG-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 2-305605
PRICH APPLICATION DATA:
                                                                                                                                                                                                 APPLICATION NUMBER: US 08/099,706
FILING DATE: 30-JUL-1993
PRIOR APPLICATION DATA:
APPLICATION UDATA: US 07/769,996
FILING DATE: 02-OCT-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/635,451
FILING DATE: 28-DEC-1990
ATTORNEY/AGENT INFORMATION:
NAME: Stevens-Smith, Theresa M.
INFORMATION FOR SEQ ID NO: 12: SEQUENCE CHARACTERISTICS: LENGTH: 2013 amino acids
                                                                                                                REGISTRATION NUMBER: 36,281
REFERENCE/DOCKET NUMBER: 90
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 659-2930
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM: MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: NON-A, NON-B HEPATITIS VIRUS GENOMIC TITLE OF INVENTION: CDNA AND ANTIGEN POLYPEPTIDE NUMBER OF SEQUENCES: 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY: U
ZIP: 20006
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: Armstrong, Westerman, Hattori, McLeland ADDRESSEE: Naughton STREET: 1725 K St. N.W. Suite 1000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         378 ALENLVYLNSASVAGAHGILSFLVFFCAAWYIKGRLVPGATYALYGVWPLLLLLLALPPR 437
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   438 AYA 440
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                                                                    440142
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                                                                                          (202) 887-0357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           YOSHIDA, Iwao
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         U.S.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OKAYAMA, Hiroto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IBM PC compatibl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Diskette, 3.5 in, 1.44Mb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Chisato
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          86.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PC-DOS/MS-DOS, Version 5.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 283; DB 3; I
Pred. No. 4.6e-28;
4; Mismatches 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 480;
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RESULT 14
US-08-384-616-12
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Best Local Similarity 85.7%;
                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/769,996
FILING DATE: 02-OCT-1991
APPLICATION NUMBER: JP 2-167466
FILING DATE: 25-JUN-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 2-230921
FILING DATE: 31-AUG-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 2-305605
FILING DATE: 09-NOV-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/635,451
APPLICATION STATE
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                                                                                                  TELEX: 440142
INFORMATION FOR SEQ ID NO: 12:
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APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
                                                                                                                                                             NAME: Stevens-Smith, Theresa M.
REGISTRATION NUMBER: 36,281
REFERENCE/DOCKET NUMBER: 900703B
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 659-2930
TELLEFAX: (202) 887-0357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDIUM TYPE: Diskette, 3.5 in, 1.44mb
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS, Version 5.0
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/384,616
                             SEQUENCE CHARACTERISTICS:
LENGTH: 2013 amino aci
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: YOSHIDA, Iwao
TITLE OF INVENTION: NON-A, NON-B HEPATITIS VIRUS
TITLE OF INVENTION: CDNA AND ANTIGEN POLYPEPTIDE
NUMBER OF SEQUENCES: 50
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        807 AYA 809
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: 2013 amino acids amino acid
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MORI, Chisato
TAKAMIZAWA, Akahisa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              U.S.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           protein
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RESULT 15
US-08-904-686A-12
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 2-305605
FILING DATE: 09-NOV-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/099,706
FILING DATE: 30-JUL-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/769,996
FILING DATE: 02-OCT-1991
PRIOR APPLICATION NUMBER: US 07/635,451
PRIOR APPLICATION NUMBER: US 07/635,451
FILING DATE: 28-DEC-1990
ATTORNEY/AGENT INFORMATION:
NAME: MCLeland, Le-Nhung
REGISTRATION NUMBER: 31,541
REFERENCE/DOCKET NUMBER: 900703G
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS, Ver
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/904,686A
FILING DATE: 01-AUG-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/324,977
APPLICATION NUMBER: US 08/324,977
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
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APPLICANT:
                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 2-
FILING DATE: 31-AUG-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: OKAYAM APPLICANT: FUKE,
                                                                                                                                                                                                                                                                                                                                                                                FILING DATE: 18-OCT-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 2-167466
FILING DATE: 25-UUN-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: NON-A, NON-B HEPATITIS VIRUS
TITLE OF INVENTION: CDNA AND ANTIGEN POLYPEPTIDE
NUMBER OF SEQUENCES: 50
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY: U
ZIP: 20006
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: Armstrong, Westerman, Hattori, McLeland ADDRESSEE: Naughton STREET: 1725 K St. N.W. Suite 1000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CITY: Washington
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OKAYAMA, Hiroto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     E: Diskette, 3.5 in, 1.44Mb
IBM PC compatible
SYSTEM: PC-DOS/MS-DOS, Version 5.0
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Pred. No. 2.5e-27;
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Result
No.
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Maximum
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Maximum Match 100%
Listing first 45 summaries
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Scoring table:
                                                                                                                                                                Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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      Score
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                                                                                                                                                                                                                                                                                          Published Applications AA:*

1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep:*

2: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*

3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*

4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*

5: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*

6: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep:*

7: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*

9: /cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pep:*

10: /cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pep:*

11: /cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pep:*

12: /cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pep:*

13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep:*

14: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep:*

16: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep:*

17: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep:*

18: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep:*

19: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep:*

19: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep:*

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10: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep:*

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21: /cgn2_6/ptodata/2/pubpaa/US10A_PUB.pep:*

22: /cgn2_6/ptodata/2/pubpaa/US10A_PUB.pep:*
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length: 2000000000
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327
   Query
Match Length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GenCore version 5.1.6 (c) 1993 - 2005 Compugen Ltd
      BB
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                                                                                                            SUMMARIES
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      Description
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82.3	82.3	82.3	82.3	82.3	82.3	82.3	82.3	82.3			٠	•	•	83.2	•	•	•	•	•					•	•					85.9		85.9	85.9
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9	16	10	10	10	10	9	16	10	10	10	10	9	20	16	15	15	15	14	13	ø	9				13	9	16	16	15	14	14	14	10
-973-025-4	-10-321-798-3	9-60-	-09-995-860-3	-995-808-3	-09-899-303-	US-09-973-025-36	21-798-	-09-995-791-4	-09-995-860-4	-09-995-808-4	-09-8	US-09-973-025-46	06-313-	-10-817-591-	-10-719-6	-10-29	-10-189-359-	-10-259-	US-10-104-966-1	US-09-747-419-20	US-09-929-955-1)-952-572-	-10-817-591-	.0-719-	-10-104-966-	09-929-95		US-10-333-449A-34	•	-10-191-966-	-10-191-966-	-10-191-966-	1
48, 1	36,	36,	36,	36,	36	36,	46	9	46	46,	e 46,	46,	e 20,	e 1,	1, Appl	406,	14,	20, App	e 1, Appl	20, Appl	1, Appl	9, Appl	5	e 5	o G	<u>ن</u>	4, 1	e 34	1, 2	16,	9, Ap	2, App	Sequence 16, Appl

ALIGNMENTS

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APPLICANT: DWEK, RAYMOND ALLEN
APPLICANT: DWEK, RAYMOND ALLEN
TITLE OF INVENTION: USE OF IMINOSUGAR DERIVATIVES TO
TITLE OF INVENTION: ACTIVITY
FILE REFERENCE: 080618-0304
CURRENT APPLICATION NUMBER: US/10/669,175
CURRENT FILING DATE: 2003-09-23
PRIOR APPLICATION NUMBER: 60/412,560
PRIOR FILING DATE: 2002-09-23
NUMBER OF SEQ ID NOS: 6
SOFTWARE: Patentin Ver. 3.2
SEQ ID NO 1
LENGTH: 63
TYPE: PRI
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence
OTHER INFORMATION: Consensus amino acid sequence fo
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                                                                                                                    Query Match
Best Local Similarity
Matches 63; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 1, Application US/10669175 Publication No. US20040110795A1 GENERAL INFORMATION:
  61 AYA 63
                                          ب
                                                             1 ALENLVVLNAASAAGTHGILWFLVFFCAAWYVKGRLVPGATYSLLGLWPLLLLLLLALPQR
                                        ALENL VYLNAASAAGTHGILWELVFFCAAWYVKGRLVPGATYSLLGLWPLLLLLLLALPQR
                                                                                                                        Conservative
                                                                                                                                                                                                                     Description of Artificial Sequence: Synthetic consensus amino acid sequence for HCV p7
                                                                                                                                           100.0%; Score 327; DB 16; 100.0%; Pred. No. 4.7e-31;
                                                                                                                        <u>.</u>
                                                                                                                          Mismatches
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US-10-669-175-1 US-09-919-901-23 US-10-191-966-23 US-09-919-901-11 US-09-919-901-11 US-09-919-901-18 US-10-191-966-11 US-10-191-966-11 US-10-191-966-11 US-09-919-901-9 US-09-919-901-9

Sequence 1, Appli Sequence 23, Appl Sequence 23, Appli Sequence 4, Appli Sequence 11, Appli Sequence 18, Appli Sequence 11, Appli Sequence 11, Appli Sequence 11, Appli Sequence 2, Applii Sequence 9, Applii

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63

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APPLICANT: Jackson, Roberta L.

APPLICANT: Jackson, Roberta L.

APPLICANT: Patick, Amy K.

APPLICANT: Patick, Amy K.

APPLICANT: Patick, Amy K.

TITLE OF INVENTION: REPORTER GENE SYSTEM FOR USE IN CELL-BASED ASSESSMENT TITLE OF INVENTION: OF INHIBITORS OF THE HEPATITIS C VIRUS PROTEASE FILE REFERENCE: 0125-0005A

CURRENT APPLICATION NUMBER: US/10/191,966

CURRENT FILING DATE: 1090-03-08

PRIOR APPLICATION NUMBER: US/09/263,933

PRIOR FILING DATE: 1999-03-08

PRIOR FILING DATE: 1999-03-08

PRIOR APPLICATION NUMBER: 09/129,611

PRIOR APPLICATION NUMBER: 09/129,611

PRIOR FILING DATE: 1998-08-05

NUMBER OF SEQ ID NOS: 33

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 23

LENGTH: 88

TYPE: PRT

ORGANISM: Artificial Sequence
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US-10-191-966-23
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CURRENT APPLICATION NUMBER: US/09/919,901
CURRENT FILING DATE: 2001-08-02
PRIOR APPLICATION NUMBER: 09/263,933
PRIOR APPLICATION NUMBER: 09/263,933
PRIOR FILING DATE: 1999-02-08
PRIOR PPLICATION NUMBER: 09/129,611
PRIOR FILING DATE: 1998-08-05
NUMBER OF SEO ID NOS: 33
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SEQ ID NO 23
LENGTH: 88
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 23, Application US/10191966 Publication No. US20030175692A1
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Potts, Karen E.
APPLICANT: Jackson, Roberta L.
APPLICANT: Jackson, Roberta L.
APPLICANT: Patisk, Amy K.
TITLE OF INVENTION: REPORTER GENE SYSTEM FOR USB IN CELL-BASED ASSESSMENT
TITLE OF INVENTION: OF INHIBITORS OF THE HEPATITIS C VIRUS PROTEASE
OTHER INFORMATION: Description of Artificial Sequence: OTHER INFORMATION: fragment of the HCV polyprotein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OTHER INFORMATION: Description of Artificial Sequence: amino acid OTHER INFORMATION: fragment of the HCV polyprotein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT ORGANISM: Artificial Sequence
                                                   FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                54;
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Pred. No. 1.1e-25;
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; LENGTH: 1692
; TYPE: PRT
                                                                                                                                                                                                                                                           Sequence 11, Application US/09919901 Publication No. US20030082518A1 . GENERAL INFORMATION:
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Best Local Similarity
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Best Local Similarity
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CURRENT APPLICATION NUMBER: US/09/919,901
CURRENT FILING DATE: 2001-08-02
PRIOR APPLICATION NUMBER: 09/263,933
PRIOR FILING DATE: 1999-02-08
PRIOR FILING DATE: 1998-08-05
PRIOR FILING DATE: 1998-08-05
NUMBER OF SEQ ID NOS: 33
                                 CURRENT APPLICATION NUMBER: US/09/919,901
CURRENT FILING DATE: 2001-08-02
PRIOR APPLICATION NUMBER: 09/263,933
PRIOR FILING DATE: 1999-02-08
PRIOR APPLICATION NUMBER: 09/129,611
PRIOR FILING DATE: 1998-08-05
                                                                                                                                            APPLICANT: Potts, Karen E.
APPLICANT: Jackson, Roberta L.
APPLICANT: Jackson, Roberta L.
APPLICANT: Patick, Amy K.
TITLE OF INVENTION: REPORTER GENE SYSTEM FOR USE IN CELL-BASED ASSESSMENT
TITLE OF INVENTION: OF INHIBITORS OF THE HEPATITIS C VIRUS PROTEASE
FILE REFERENCE: 0125-0005A
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NUMBER OF SEQ ID NOS: 33
SOFTWARE: PatentIn Ver. 2.0
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nilarity 85.7%;
Conservative
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Pred. No. 3.7e-24;
3; Mismatches 6;
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Pred. No. 1.1e-25;
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US-09-919-901-18
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                                                                                                                                                                                          US-10-191-966-4
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Sequence 4, Application US/10191966
publication 0. US20030175692A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Potts, Karen E.
APPLICANT: Jackson, Roberta L.
APPLICANT: Patick, Amy K.
TITLE OF INVENTION: REPORTER GENE SYSTEM FOR USE IN CELL-BASED ASSESSMENT
TITLE OF INVENTION: OF INFIBITORS OF THE HEPATITIS C VIRUS PROTEASE
FILE REFERENCE: 0125-0005A
CURRENT APPLICATION NUMBER: US/10/191,966
CURRENT FILING DATE: 2002-07-10
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CURRENT FILING DATE: 2001-08-02
PRIOR APPLICATION NUMBER: 09/263,933
PRIOR FILING DATE: 1999-02-08
PRIOR APPLICATION NUMBER: 09/129,611
PRIOR FILING DATE: 1998-08-05
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APPLICANT: Jackson, Roberta L.
APPLICANT: Patick, Amy K.
APPLICANT: Patick, Amy K.
TITLE OF INVENTION: REPORTER GENE SYSTEM FOR USE IN CELL-BASED ASSESSMENT
TITLE OF INVENTION: OF INHIBITORS OF THE HEPATITIS C VIRUS PROTEASE
FILE REFERENCE: 0125-0005A
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OTHER INFORMATION: :
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85.7%;
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Pred. No. 3.7e-24;
3; Mismatches 6;
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Pred. No. 3.7e-24;
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RESULT 9
US-10-191-966-18
; Sequence 18, Application US/10191966
; Publication No. US20030175692A1
; GENERAL INFORMATION:
; APPLICANT: POTTS, Karen E.
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LENGTH: 1692
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SEQ ID NO 4
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APPLICANT: Jackson, Roberta L.
APPLICANT: Patick, Amy K.
APPLICANT: Patick, Amy K.
TITLE OF INVENTION: REPORTER GENE SYSTEM FOR USE IN CELL-BASED ASSESSMENT
TITLE OF INVENTION: OF INHIBITORS OF THE HEPATITIS C VIRUS PROTEASE
FILE REFERENCE: 0125-0005A
FILE REFERENCE: 0125-0005A
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PRIOR FILING DATE: 1999-03-08
PRIOR APPLICATION NUMBER: 09/129,611
PRIOR FILING DATE: 1998-08-05
NUMBER OF SEQ ID NOS: 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION NUMBER: US/10/191,966
CURRENT FILING DATE: 2002-07-10
PRIOR APPLICATION NUMBER: US/09/263,933
PRIOR FILING DATE: 1999-03-08
PRIOR APPLICATION NUMBER: 09/129,611
PRIOR FILING DATE: 1998-08-05
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85.7%;
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 Mismatches

 Mismatches

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Pred. No. 3.7e-24;
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Pred. No. 3.7e-24;
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FILE REFERENCE: 0125-0005A
CURRENT APPLICATION NUMBER: US/10/191,966
CURRENT FILING DATE: 2002-07-10
PRIOR APPLICATION NUMBER: US/09/263,933
PRIOR APPLICATION NUMBER: US/09/263,933
PRIOR APPLICATION NUMBER: 09/129,611
PRIOR FILING DATE: 1998-08-05
NUMBER OF SEQ ID NOS: 33
SOFTWARE: PATENTIN Ver. 2.0
SEQ ID NO 18
LENGTH: 1692
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SEQ ID NO 2
LENGTH: 2307
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Publication No. US20030082518A1
                                                                                                                                                                  Query Match
Best Local Similarity
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION NUMBER: 09/263,933
PRIOR FILING DATE: 1999-02-08
PRIOR APPLICATION NUMBER: 09/129,611
PRIOR FILING DATE: 1998-08-05
NUMBER OF SEQ ID NOS: 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Jackson, Roberta L.
APPLICANT: Patick, Amy K.
TITLE OF INVENTION: REPORTER GENE SYSTEM FOR USE IN CELL-BASED ASSESSMENT
TITLE OF INVENTION: OF INHIBITORS OF THE HEPATITIS C VIRUS PROTEASE
FILE REFERENCE: 0125-0005A
CURRENT FILING DATE: 2001-08-02
CURRENT FILING DATE: 2001-08-02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Potts, Karen E.
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TITLE OF INVENTION: REPORTER GENE SYSTEM FOR USE IN CELL-BASED ASSESSMENT
TITLE OF INVENTION: OF INHIBITORS OF THE HEPATITIS C VIRUS PROTEASE
                                                                                                                                                                                                                                                                         TYPE: PRT ORGANISM: Artificial Sequence
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                                                                                                                                                                                                                                                                  FEATURE:
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                                                                        118 ALENLVVLNAASVAGAHGILSFLVFFCAAWYIKGRLVPGAAYALYGVWPLLLLLLALPPR 177
                                                                                                                                                  54; Conservative
                                     61 AYA 63
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                                                                                                                                                                  85.9%;
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                                                                                                                                                Score 281; DB 10; Length 2307; Pred. No. 5.1e-24; 3; Mismatches 6; Indels 0
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SEQ ID NO 16
LENGTH: 2307
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
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APPLICANT: Potts, Roberta L.

APPLICANT: Jackson, Roberta L.

APPLICANT: Patick, Amy K.

TITLE OF INVENTION: REPORTER GENE SYSTEM FOR TITLE OF INVENTION: OF INHIBITORS OF THE HE FILE REFERENCE: 0125-005A

CURRENT APPLICATION NUMBER: US/09/919,901

CURRENT FILING DATE: 2001-08-02

PRIOR APPLICATION NUMBER: 09/263,933

PRIOR FILING DATE: 1999-02-08

PRIOR APPLICATION NUMBER: 09/129,611

PRIOR FILING DATE: 1998-08-05

NUMBER OF SEQ ID NOS: 33

SOFTWARE: PATENTIN PATENTIAL OF SEQ ID NOS: 33

SOFTWARE: PATENTIAL OF SEQ ID NOS: 33

SOFTWARE: PATENTIAL OF SEQ ID NOS: 33
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US-09-919-901-9
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Publication No. US20030082518A1
GENERAL INFORMATION:
                     Query Match
Best Local Similarity
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Publication No. US20030082518A1
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Best Local S
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CURRENT FILING DATE: 2001-08-02
PRIOR APPLICATION NUMBER: 09/263,933
PRIOR FILING DATE: 1999-02-08
PRIOR APPLICATION NUMBER: 09/129,611
PRIOR APPLICATION NUMBER: 09/129,611
PRIOR FILING DATE: 1998-08-05
NUMBER OF SEQ ID NOS: 33
                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Potts, Karen E.
APPLICANT: Jackson, Roberta L.
APPLICANT: Patick, Amy K.
TITLE OF INVENTION: REPORTER GENE SYSTEM FOR USE IN CELL-BASED ASSESSMENT
TITLE OF INVENTION: OF INHIBITORS OF THE HEPATITIS C VIRUS PROTEASE
FILE REFERENCE: 0125-0005A
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TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
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REPORTER GENE SYSTEM FOR USE IN CELL-BASED ASSESSMENT
OF INHIBITORS OF THE HEPATITIS C VIRUS PROTEASE
                     85.9%;
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85.7%; Pred. No. 5.1e-24;
tive 3; Mismatches 6; Indels 0
Score 281; DB 10;
Pred. No. 5.1e-24;
3; Mismatches 6;
                                          Length 2307;
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Matches

54; Conservative

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Indels

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Gaps

1 ALENLVVLNAASAAGTHGILWFLVFFCAAWYVKGRLVPGATYSLLGLWPLLLLLLALPQR 60

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APPLICANT: Jackson, Roberta L.

APPLICANT: Jackson, Roberta L.

APPLICANT: Jackson, Roberta L.

APPLICANT: Patick, Amy K.

APPLICANT: Patick, Amy K.

TITLE OF INVENTION: REPORTER GENE SYSTEM FOR USE IN CELL-BASED ASSESSMENT TITLE OF INVENTION: OF INHIBITORS OF THE HEPATITIS C VIRUS PROTEASE FILE REFERENCE: 0125-0005A

CURRENT APPLICATION NUMBER: US/10/191,966

CURRENT FILING DATE: 2002-07-10

PRIOR APPLICATION NUMBER: US/99/263,933

PRIOR APPLICATION NUMBER: US/99/263,933

PRIOR APPLICATION NUMBER: US/99/263,933

PRIOR APPLICATION NUMBER: 09/129,611

PRIOR APPLICATION NUMBER: 09/129,611

PRIOR FILING DATE: 1998-08-05

NUMBER OF SEQ ID NOS: 33

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 9

LENGTH: 2307

TYPE: PRT
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US-10-191-966-2
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US-10-191-966-2
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LENGTH: 2307
TYPE: PRT
ORGANISM: Artificial Sequence
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Best Local Similarity
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APPLICANT: Jackson, Roberta L.
APPLICANT: PATICK, AMY K.
APPLICANT: PATICK, AMY K.
TITLE OF INVENTION: REPORTER GENE SYSTEM FOR USE IN CELL-BASED ASSESSMENT TITLE OF INVENTION: OF INHIBITORS OF THE HEPATITIS C VIRUS PROTEASE FILE REFERENCE: 0125-005A
CURRENT FILING DATE: 2002-07-10
PRIOR APPLICATION NUMBER: US/09/263,933
PRIOR FILING DATE: 1999-03-08
PRIOR APPLICATION NUMBER: US/09/263,933
PRIOR APPLICATION NUMBER: US/09/263,933
PRIOR APPLICATION NUMBER: US/09/263,933
PRIOR FILING DATE: 1999-03-08
PRIOR FILING DATE: 1999-03-08
PRIOR APPLICATION NUMBER: 09/129,611
PRIOR FILING DATE: 1998-08-05
NUMBER OF SEQ ID NOS: 33
SOFTWARE: PATENTIN Ver. 2.0
FEATURE:
OTHER INFORMATION: :
                                               ORGANISM: Artificial Sequence
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85.7%;
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SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 16
LENGTH: 2307
TYPE: PRT
OTRANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: :
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Search completed: October Job time : 166 secs
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US-10-191-966-16
Sequence 16, Application US/10191966
; Publication No. US20030175692A1
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Best Local Similarity
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Best Local Similarity
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APPLICANT: Jackson, Roberta L.
APPLICANT: Jackson, Roberta L.
APPLICANT: Jackson, Roberta L.
APPLICANT: Patick, Amy K.
APPLICANT: Patick, Amy K.
APPLICANT: Patick, Amy K.
APPLICANT: Patick, Amy K.
APPLICATION: Patick SYSTEM FOR USE IN CELL-BASED ASSESSMENT
TITLE OF INVENTION: OF INHIBITORS OF THE HEPATITIS C VIRUS PROTEASE
FILE REFERENCE: 0125-005A
CURRENT APPLICATION NUMBER: US/10/191,966
CURRENT FILING DATE: 1999-03-08
PRIOR APPLICATION NUMBER: US/09/263,933
PRIOR APPLICATION NUMBER: 09/129,611
PRIOR FILING DATE: 1998-08-05
NUMBER OF SEQ ID NOS: 33
NUMBER OF SEQ ID NOS: 33
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                                                                                                       61 AYA
                                                                                                                                                                                                          11 Similarity 85.7%;
54; Conservative
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                                                                     AYA 180
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                  4, 2005, 19:01:35
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Pred. No. 5.1e-24;
3; Mismatches 6;
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Pred. No. 5.1e-24;
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Total number of hits satisfying chosen parameters:
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Perfect score:
Post-processing: Minimum Match 0%
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Listing first 45 summaries
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327
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Copyright (c) 1993 - 2005 Compugen Ltd.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Database

PIR 79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

SUMMARIES

5	44	3	42	41	40	9	38	37	36	υ 5	34 4	ü	32	31	30
59	59.5	59.5	59.5	59.5	59.5	60	60	60	60	60	60	60	60.5	60.5	60.5
18.0	18.2	18.2	18.2	18.2	18.2	18.3	18.3	18.3	18.3	18.3	18.3	18.3	18.5	18.5	18.5
133	665	516	516	283	219	1085	459	400	400	341	326	285	1337	454	414
N	N	N	N	N	N	N	N	N	N	N	N	N	N	N	-
PH0210	C81439	G98198	AB3088	E71310	H75342	H82511	H83675	A53281	A41679	E96019	T30166	T12342	T38949	AD2460	QRHUB3
hypothetical prote	probable integral	proline/betaine tr	MFS permease [prol	conserved hypothet	probable hemolysin	hypothetical prote	hypothetical prote	beta 3-adrenergic	beta-3-adrenergic	probable sugar upt	hypothetical prote .	major intrinsic pr	hypothetical prote	hypothetical prote	beta-3-adrenergic .

ALIGNMENTS

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A;Crost references; EMBL;K61591
A;Note: this sequence is inconsistent with the nucleotide translation
A;Note: the authors translated the codon AGG for residue 43 as Pro, TGG for residue 320
A;Note: sequence extracted the codon AGG for residue 43 as Pro, TGG for residue 771 as Ser
A;Note: sequence extracted from NCBI backbone (NCBIN:121747, NCBIP:121748)
C;Superfamily: hepatitis C virus genome polyprotein
C;Keywords: ATP; glycoprotein; hydrolase; nucleotide binding; P-loop; polyprotein; serir
F;2-115/Product: capsid protein C #status predicted <CPC>
F;116-191/Product: major envelope protein M #status predicted <MEE>
F;390-729/Product: nonstructural protein NS2 #status predicted <NS1>
F;390-729/Product: nonstructural protein NS2 #status predicted <NS2>
F;1207-1615/Product: hepacivirin #status predicted <NS3>
F;1230-1237/Region: nucleotide-binding motif B
F;1616-1862/Product: nonstructural protein NS4a #status predicted <N4A>
F;1863-2013/Product: nonstructural protein NS4a #status predicted <N4B>
F;2014-3010/Product: nonstructural protein NS5 #status predicted <NS5>
F;2014-3010/Product: nonstructural protein NS5 #status predicted <NS5>
F;196,209,234,250,305,417,423,448,532,540,556,576,623,645/Binding site: carbohydrate (A
                                                                                                                                                                                                                                 genome polyprotein - hepatitis C virus (strain J)
N;Contains: capsid protein C; envelope protein M; major envelope protein NS4a; nonstructural protein NS4b; nonstructural protein IC;Species: hepatitis C virus
C;Species: hepatitis C virus
C;Date: 30-Jun-1992 #sequence revision 30-Jun-1992 #text_change 0:
C;Accession: A39253; PS0086
R;Kato, N.; Hijikata, M.; Ootsuyama, Y.; Nakagawa, M.; Ohkoshi, S
Proc. Natl. Acad. Sci. U.S.A. 87, 9524-9528, 1990
A;Title: Molecular cloning of the human hepatitis C virus genome:
A;Accession: A39253; MUID:91088550; PMID:2175903
A;Accession: A39253
                                                   A;Cross-references: UNIPROT:P26662; GB:D90208; R;Kato, N.; Ohkoshi, S.; Shimotohno, K. Proc. Jpn. Acad. 65B, 219-223, 1989
A;Title: Japanese isolates of the non-A, non-B
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A;Residues: 1-3010 <HON>
A;Residues: 1-3010 <HON>
A;Residues: 1-3010 <HON>
A;Cross-references: UNIPROT:Q68949; EMBL:X61596; NID:g59478; PIDN:CAA43793.1;
A;Experimental source: isolate JK1 from an individual
R;Honda, M.; Kaneko, S.; Unoura, M.; Kobayashi, K.; Murakami, S.
Arch. Virol. 128, 163-169, 1993
A;Title: Sequence analysis of putative structural regions of hepatitis C virus
A;Reference number: A48332; MUID:93119270; PMID:8380322
A;Accession: S33570
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A; Reference a A; Accession:
                                                                                                                                                                                    A; Molecule type: genomic RNA
A; Residues: 1-3010 < KAT>
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A;Residues: 1-547,'T',549-621,'V',623-624,'S',626-652,'DL',655-761,'T',763-782
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;Accession: $18030; $33570; Ā4833; $18029
;Honda, M.; Kaneko, S.; Masaabi, U.; Kobayashi, K.; Murakami, S.
ubmitted to the EMBL Data Library, September 1991
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ALENLVVLNAASAAGTHGILWFLVFFCAAWYVKGRLVPGATYSLLGLWPLLLLLLLALPQR
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Pred. No. 4.4e-23;
""" anatches 7;
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A;Reference number: A41546; MUID:92052256; PMID:1658800
A;Contents: annotation
A;Contents: annotation
C;Superfamily: hepatitis C virus genome polyprotein
C;Superfamily: hepatitis C virus genome polyprotein
C;Keywords: ATP; capsid protein; envelope protein; glycoprotein; hyd.
F;1-115/Product: envelope protein M #status predicted <CPC>
F;116-191/Product: major envelope protein B #status predicted <EBM>
F;192-389/Product: monstructural protein NS1 #status predicted <NEE>
F;300-729/Product: nonstructural protein NS1 #status predicted <NS1>
F;301-106/Product: nonstructural protein NS2 #status predicted <NS1>
F;1007-1615/Product: hepacivirin #status predicted <NS3>
F;1030-1237/Region: nucleotide-binding motif A (P-loop)
F;311-3137/Region: nucleotide-binding motif B
F;311-319/Region: DEXH motif
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F;192-389/Product: major envelope protein E #status predicted <-
F;390-729/Product: nonstructural protein NS1 #status predicted <-
F;730-1006/Product: nonstructural protein NS2 #status predicted <-
F;730-1615/Product: hepacivirin #status predicted <-
F;1007-1615/Product: hepacivirin #status predicted <-
F;1230-1237/Region: nucleotide-binding motif A (P-loop)
F;1312-1317/Region: bEXH motif
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Molecule type: genomic RNA
A;Residues: 1-3011 <INC>
A;Residues: 1-3011 <INC>
A;Cross references: UNIPROT:P27958; GB:M67463; NID:g329737; PIDN:AAA45534.1;
A;Cross references: UNIPROT:P27958; GB:M67463; NID:g329737; PIDN:AAA45534.1;
R;Inchauspe, G; Zebedee, S.; Lee, D.H.; Sugitani, M.; Nasoff, M.; Prince, A.
Proc. Natl. Acad. Sci. U.S.A. 88, 10292-10296, 1991
A;Title: Genomic structure of the human prototype strain H of hepatitis C vir
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT
GNWVCH
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F;1616-1862/Product: nonstructural protein NS4a #status predicted <N4A>F;1863-2013/Product: nonstructural protein NS4b #status predicted <N4B>F;2014-3011/Product: nonstructural protein NS5 #status predicted <N4S>F;2014-3011/Product: nonstructural protein NS5 #status predicted <NS5>F;196,209,234,305,325,417,423,430,448,476,532,540,556,576,623,645,1213,
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A;Description: Genomic structure of the h
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N;Contains: capsid protein C; envelope protein M; hepacivirin (EC 3.4.21.98) (nonstructu
protein NS4a; nonstructural protein NS4b; nonstructural protein NS5
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A; Residues: 2650-2707 < KA2>
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Pred. No. 7.3e-23;
4; Mismatches 6
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   edicted <NS5>,623,645,1213,1255
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   2041,2240,
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Score

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Length

Best Local Similarity

81.0%;

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A;Note: Bequence extracted from NCBI backbone (NCBIN:106206, NCBIP:106207)
C;Superfamily: hepatitis C virus genome polyprotein
C;Keywords: ATP; glycoprotein; hydrolase; nucleotide binding; P-loop; poly;
F;2-115/product: capsid protein C #status predicted <CPC>
F;116-191/product: envelope protein M #status predicted EPM>
F;192-389/product: major envelope protein E #status predicted <MEE>
F;390-729/product: nonstructural protein NS1 #status predicted <NS1>
F;730-1006/Product: nonstructural protein NS1 #status predicted <NS1>
F;1307-1615/product: hepacivirin #status predicted <NS2>
F;1230-1237/Region: nucleotide-binding motif B
F;1312-1317/Region: DEXH motif
F;1315-1319/Region: DEXH motif
CiAccession: A40244
CiAccession: A40244
RiChen, P.J.; Lin, M.H.; Tai, K.F.; Liu, P.C.; Lin, C.J.; Chen, D.S.
Virology 188, 102-113, 1992
A;Title: The Taiwanese hepatitis C virus genome: sequence determination and mapping the A;Reference number: A40244; MUID:92230206; PMID:1314449
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N;Contains: capsid protein C; envelope protein M; hepacivirin (EC 3.4.21.98) (nonstructu protein NS4s; nonstructural protein NS5 C;Species: hepatitis C virus
C;Species: hepatitis C virus
C;Date: 19-May-2000 #sequence_revision 19-May-2000 #text_change 09-Jul-2004
C:Accessin. A4:273
                                                                                                                                                                                                          genome polyprotein - hepatitis C virus (strain Taiwan)
N;Contains: capsid protein C; envelope protein M; hepacivirin (EC 3.4.21.98) (nonstructus
protein NS4a; nonstructural protein NS5
C;Species: hepatitis C virus
A;Note: host Homo sapiens (man)
C;Date: 31-DeC-1992 #sequence_revision 31-Dec-1992 #text_change 09-Jul-2004
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Virus Res. 23, 39-53, 1992
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A;Reference number: A45573; MUID:92295714; PMID:1318627
A;Accession: A45573
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A; Residues: 1-3010 < TAN>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 ALENLYVLNAASAAGTHGILWFLVFFCAAWYVKGRLVPGATYSLLGLWPLLLLLLLALPQR 60
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Pred. No. 2.1e-22;
3; Mismatches 7;
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A; Molecule type: genomic RNA
A; Residues: 1577-1633 cCH2>
A; Experimental source: isolates E-bl7
C; Superfamily: hepatitis C virus genome polyprotein
C; Keywords: ATP; capsid protein; envelope protein; glycoprotein; hydrol
F;11-115/Product: capsid protein C #status predicted <CPC>
F;116-191/Product: envelope protein M #status predicted <EPM>
F;12-389/Product: major envelope protein E #status predicted <MEE>
F;390-729/Product: nonstructural protein NS1 #status predicted <NS1>
F;300-1006/Product: nonstructural protein NS2 #status predicted <NS1>
F;1007-1615/Product: hepacivirin #status predicted <NS2>
F;1230-1237/Region: nucleotide-binding motif A (P-loop)
F;1312-3137/Region: DEXH motif
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A; Residues: 1-3010 < CCHS
A; Cross-references: UNIPROT: P29846; GB: M84754
C; Superfamily: hepatitis C virus genome polyprotein; glycoprotein; hydrolase; l? (Expwords: ATP; capsid protein; envelope protein; glycoprotein; hydrolase; l?; 1-15/Product: capsid protein C #status predicted <CPC>F; 116-191/Product: envelope protein M #status predicted <EPM>F; 192-389/Product: major envelope protein B #status predicted <NS1>F; 390-729/Product: nonstructural protein NS1 #status predicted <NS1>F; 730-1006/Product: nonstructural protein NS2 #status predicted <NS2>F; 1007-1615/Product: hepacivirin #status predicted <NS3>F; 1031-1337/Region: nucleotide-binding motif A (P-loop)
F; 3116-1319/Region: DEXH motif
F; 151616-1852/Product: DEXH motif
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J. Gen. Virol. 73, 1131-1141, 1992
A;Title: Analysis of a new hepatitis C virus type and its phylogenetic relationship to A;Reference number: PQ0393; MUID:92268871; PMID:1316939
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C;Date: 30-Sep-1992 #sequence revision 30-Sep-1992 #text_change 09-Jul-2004 C;Accession: A39166; PQ0403; PQ0404 R;Choo, Q,L.; Richman, K.H.; Han, J.H.; Berger, K.; Lee, C.; Dong, C.; Gallegos, Proc. Natl. Acad. Sci. U.S.A. 88, 2451-2455, 1991 A;Title: Genetic organization and diversity of the hepatitis C virus. A;Reference number: A39166; MUID:91172826; PMID:1848704 A;Accession: A39166.
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N;Contains: capsid protein C; envelope protein M; hepacivirin (EC 3.4.21.98) (nonstructu
protein NS4a; nonstructural protein NS4b; nonstructural protein NS5
C;Species: hepatitis C virus
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F;1863-2013/Product: nonstructural protein NS4b #status predicted <N4B>
F;2014-3010/Product: nonstructural protein NS5 #status predicted <N85>
F;2014-3010/Product: nonstructural protein NS5 #status predicted <N85>
F;196,209,233,234,250,305,325,417,423,430,448,532,540,556,576,623,645,1213,1255,2041,207
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A;Experimental source: isolates
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A; Residues: 1577-1633 < CHA>
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A; Residues: 1-3011 < CHO>
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52; Conservative
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Pred. No. 2.1e-22;
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E.; Yap, P.L
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RESULT
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A;Cross-references: UNIPROT:003463; EMBL:D10749; NID:g22158
A;Cross-references: UNIPROT:003463; EMBL:D10749; NID:g22158
A;Okamoto, H.; Okada, S.; Sugiyama, Y.; Yotsumoto, S.; Tana
pn. J. Exp. Med. 60, 167-177, 1990
A;Title: The 5'-terminal sequence of the hepatitis C virus
A;Reference number: PC1284; MUID:91013116; PMID:2170712
A;Accession: PC1285
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N;Contains: capsid protein C; envelope protein M; hepacivirin (EC 3.4.21.98
protein NS4a; nonstructural protein NS4b; nonstructural protein NS5
C;Species: hepatitis C virus
C;Date: 19-May-2000 #sequence_revision 19-May-2000 #text_change 09-Jul-2004
genome
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               R;Okamoto, H.
submitted to the EMBL Data Library, March
A;Reference number: $40770
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F;1312-1317/Region: pucleotide-binding motif B
F;1316-1319/Region: DEXH motif
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S40770
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F;1863-2013/Product: nonstructural protein NS4b #status predicted <N4B>
F;2014-3011/Product: nonstructural protein NS5 #status predicted <NS5-
F;2014-3011/Product: nonstructural protein NS5 #status predicted <NS5-
F;196,209,234,305,325,417,423,430,448,476,532,540,556,576,623,645,1213,1255,2041,2077,22
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A; Residues: 1-513 < OK2>
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Matches 50
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                                                                                                                                                                                    AYA 63
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llarity 79.4%;
Conservative
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77.8%;
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  virus
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Pred. No. 1.3e-21;
Mismatches 7;
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Pred. No. 9.9e-22;
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  (strain
  HC-J8)
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H.; Tsuda,
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                                                                                                                                                                                                       genome polyprotein - hepatitis C virus (isolate HC-J6) N;Contains: capsid protein C; envelope protein M; hepaciprotein NS4a; nonstructural protein NS4b; nonstructural C;Species: hepatitis C virus
                                                 R;Okamoto, H.; Okada, S.; Sugiyama, Y.; Kurai, K.; Iizuka, H.
J. Gen. Virol. 72, 2697-2704, 1991
A;Title: Nucleotide sequence of the genomic RNA of hepatitis
A;Reference number: JQ1303; MUID:92044440; PMID:1658196
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                        A; Accession: JQ1303
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751 ALEKLIILHSASAASANGPLWFFIFFTAAWYLKGRVVPVATYSVLGLWSFLLLVLALPQQ

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AYA 63

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19-May-2000

K.; Iizuka, H.; Machida, A.; Miyakawa,

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isolated

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#text_change 09-Jul-2004 protein

protein M; hepacivirin (EC 3.4.21.98)

(nonstructu

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A,Experimental source: isolate E-bl2
R;Kato, N.; Ootsuyama, Y.; Ohkoshi, S.; Nakazawa, T.; M.
Biochem. Biophys. Res. Commun. 181, 279-285, 1991
A;Title: Distribution of plural HCV types in Japan.
A;Reference number: PQ0554; NUID:92068204; PMID:1720309
A;Accession: PQ0559
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A;Title: Full-length sequence of a hepatitis C virus A;Reference number: A40250; MUID:92230232; PMID:13144
A;Accession: A40250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       J. Gen. Virol. 73, 1131-1141, 1992
J. Gen. Virol. 73, 1131-1141, 1992
A;Title: Analysis of a new hepatitis C virus type and its
A;Title: Analysis of a new human MIID:92268871; PMID:1316939
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A;Residues: 1-3033 <OKA>
A;Cross-references: UNIPROT:P26661; GB:D10988; GB:D01221; NID:g221608; PIDN:BAA01761.1;
A;Chan, S.W.; McOmish, F.; Holmes, E.C.; Dow, B.; Peutherer, J.F.; Follett, E.; Yap, P.L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Molecule type: genomic RNA
A; Residues: 2678-2754 < CHA>
A; Cross-references: DDBJ:D10134
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C;Date: 31-Dec-1992 #sequence revision 31-Dec-1992 #text_change 09-Jul-2004
C;Accession: A40250; PQ0397; PQ0559
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                                                                       Query Match
Best Local
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                                                                         Similarity
ALENLVVLNAASAAGTHGILWFLVFFCAAWYVKGRLVPGATYSLLGLWPLLLLLLLALPQR
                                                      Conservative
                                                                         71.6%;
                                                        11;
                                                    Score 234; DB 1; Length 3033; 
Pred. No. 3.2e-18; 
1; Mismatches 9; Indels
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A;Residues: 1-3033 <OKA>
A;Cross-references: UNIPROT: D26660; GB:D00944; NID: 9221650; PIDN:BAA00792.1; PID: 9221651
A;Experimental source: isolate HC-J6 from a Japanese individual
C;Superfamily: hepatitis C virus genome polyprotein
C;Keywords: ATP; glycoprotein; hydrolase; P-loop; polyprotein; serine proteinase; transm
F;2-115/Product: capsid protein C #status predicted <CPC>
F;116-191/Product: envelope protein M #status predicted <AMES>
F;190-733/Product: nonstructural protein NS1 #status predicted <NS2>
F;390-733/Product: nonstructural protein NS2 #status predicted <NS2>
F;1011-1619/Product: hepacivirin #status predicted <NS2>
F;1011-1619/Product: hepacivirin #status predicted <NS2>
F;1316-1321/Region: nucleotide-binding motif B
F;1320-1323/Region: DEXH motif
F;1667-2017/Product: nonstructural protein NS4s #status predicted <N4B>
F;1067-2017/Product: nonstructural protein NS4s #status predicted <N4B>
F;1067-2017/Product: nonstructural protein NS4s #status predicted <N059
F;1018-033/Product: nonstructural protein NS5 #status predicted <N059
F;1018-033/Product: nonstructural protein NS64s #status predicted <N059
F;1018-033/Product: nonstructural protein NS5 #status predicted <N059
F;1018-033/Product: nonstructural protein NS64s #status predicted 
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N;Contains: capsid protein C; envelope protein M; hepacivirin (EC 3.4.21.98)
protein NS4a; nonstructural protein NS4b; nonstructural protein NS5
C;Species: hepatitis C virus
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A;Tille: The complete coding sequence of hepatitis C virus genotype 5a, the predominant
A;Reference number: JC5620; MUID:97366593; PMID:9223423
A;Accession: JC5620
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Similarity 71.4%;
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   KNVIVLNAAAAAGNHGFFWGLLVVCLAWHVKGRLVPGATYLCLGVWPLLLVRLLRPHRAL
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                                                                                                                                        Score 212; DB 1;
Pred. No. 9.9e-16;
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                                                                                                               Mismatches
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                                                                                                                                                                   Length 3014;
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   RESULT 14
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A;Description: Sequence analysis
A;Reference number: S18029
A;Accession: S18032
A;Molecule type: genomic RNA
A;Residues: 1-782 <HON>
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C;Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change C;Accession: S18032
R;Honda, M.; Kaneko, S.; Masashi, U.; Kobayashi, K.; Murakami, submitted to the EMBL Data Library, September 1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Cross-references: UNIPROT:068953; EMBL:X61595; NID:959486; PIDN:CAA43792.1; A; Experimental source: isolate JK5
C; Superfamily: hepatitis C virus genome polyprotein
C; Keywords: capsid protein; core protein; envelope protein; glycoprotein; nons
F;1-191/Product: core protein #status predicted <MAT1>
F;192-383/Product: envelope protein #status predicted <MAT2>
F;384-733/Product: NS1/E2 protein #status predicted <MAT3>
F;734-782/Product: nonstructural protein 2 (fragment) #status predicted <MAT4>
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                                                                                                                                                                                                                                                                                                                                                     A;Experimental source: isolate JK4
C;Superfamily: hepatitis C virus genome polyprotein
C;Superfamily: hepatitis C virus genome polyprotein; glycoprotein; nonstructural
C;Keywords: capsid protein; core protein; envelope protein #Status predicted cMAT1>
F;1-191/Product: core protein #Status predicted cMAT2>
F;392-383/Product: envelope protein 1 #Status predicted cMAT3>
F;394-733/Product: NSI/E2 protein #Status predicted cMAT3>
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A; Residues: 1-782 < HON>
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Numberintion: Sequence analysis of putative structural regions of Hepatitis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 09-Jul-2004;
Accession: S18032
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Best Local Similarity
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                                                         ALENLVVLNAASAAGTHGILWFLVFFCAAWYVKGRL 36
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L Data Library, September 1991
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Pred. No. 4.6e-11;
l; Mismatches 3
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1, nonstructural protein 2; NS1/E2
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hypothetical protein 787 - hepatitis C virus (fragment)
C;Species: hepatitis C virus
C;Species: hepatitis C virus
C;Date: 14-Jul-1994 #sequence_revision 14-Jul-1994 #text_change 09-Jul-2004
C;Accession: PN0677
R;Cho, S.H.; Yoon, J.I.; Chang, J.E.; Ahn, B.M.; Lee, C.H.; Lee, Y.I.
Blochem. Biophys. Res. Commun. 196, 780-788, 1993
A;Title: Genomic typing of hepatitis C viruses from Korean patients: Implications of A;Reference number: PN0677; MUID:94059104; PMID:8240354
A;Accession: PN0677; MUID:94059104; PMID:8240354
                                                                                                                                                                                                                                                                                                                             A;Cross-references: UNIPROT:068951; EMBL:X61592; NID:g59482; PIDN:CAA43789.1; PID:g59483; A;Experimental source: isolate JK3
C;Superfamily: hepatitis C virus genome polyprotein
C;Keywords: capsid protein; core protein; envelope protein; glycoprotein; nonstructural
F;1-191/Product: core protein #status predicted <MAT1>
F;192-383/Product: envelope protein 1 #status predicted <MAT2>
F;384-733/Product: NS1/E2 protein #status predicted <MAT3>
F;734-782/Product: nonstructural protein 2 (fragment) #status predicted <MAT4>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        genome polyprotein - hepatitis C virus (isolate JK3) (fragment)
N;Contains: core protein; envelope protein 1; nonstructural protein 2; NS1/E2 protein
C;Species: hepatitis C virus
A;Variety: isolate JK3
C;Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 09-Jul-2004
C;Accession: S19875
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A;Residues: 1-787 cCIO>
A;Cross-references: UNIPROT:Q08244; GB:L20498; NID:g1381031; PIDN:AAB02608.1; PID:g13810
C;Superfamily: hepatitis C virus genome polyprotein
C;Keywords: glycoprotein; nonstructural protein
E;196,209,234,250,305,325,421,427,452,536,544,560,580,627,649/Binding site: carbohydrate
Search completed: October 4, 2005, 18:57:53 Job time : 16 secs
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A; Residues: 1-782 <HON>
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Best Local S
Matches 31
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Best Local Similarity 83.8
Matches 31; Conservative
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||||||||||||| || 78
47 ALENLVVLNAASVAGTRGIPFFLVFFCAAWYIKGRL 78
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Pred. No. 2.2e-10;
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Pred. No. 1.7e-10;
2; Mismatches 4
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Maximum DB
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Perfect score:
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Q8V638
Q9J3F9
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(without alignments)
512.079 Million cell updates/sec
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      Q9qix4
Q9qpix1
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Q9qmx2
Q9dtdde
Q9dtdde
Q9d3g0
Q9j3g0
Q9j3g1
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Q8v638
Q9j3f9
Q9j3f9
Q9qix3
Q9qp91
Q6gp91
Q68826
Q6gyr9
Q9dte1
Q9j3g3
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Q68533
Q9j3g8
Q9j3h1
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      7 hepatitis cable partitis cable par
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Q9J3H7
          R GO; GO:0016021; C:integral to membrane; IEA.
R GO; GO:001902B; C:viral capaid; IEA.
R GO; GO:001902B; C:viral envelope; IEA.
R GO; GO:001902B; C:viral envelope; IEA.
R GO; GO:0005524; F:ATP binding; IEA.
R GO; GO:0005524; F:ATP binding; IEA.
R GO; GO:0003722; F:NA binding; IEA.
R GO; GO:0003723; F:NA binding; IEA.
R GO; GO:0003526; F:RNA-directed RNA polymerase activity; IEA.
R GO; GO:0003528; F:serine-type peptidase activity; IEA.
R GO; GO:0005298; F:structural molecule activity; IEA.
R GO; GO:0005198; F:structural molecule activity; IEA.
R GO; GO:0005198; F:proteolysis and peptidolysis; IEA.
R GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
R GO; GO:0006350; P:transcription; IEA.
R GO; GO:0006350; P:transcription; IEA.
R GO; GO:0019079; P:viral genome replication; IEA.
R GO; GO:0019079; P:viral transformation; IEA.
R GO; GO:0019079; P:viral transformation; IEA.
R InterPro; IPR001410; DEAD.
R InterPro; IPR001410; DEAD.
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Q9J3H7;
01-OCT-2000 (TrEMBLrel. 1
01-OCT-2000 (TrEMBLrel. 1
01-MAR-2004 (TrEMBLrel. 2
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Pfam; PF01
Pfam; PF01
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InterPro;
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Submitted (NOV-1999) to the
EMBL; AF207756; AAF65946.1;
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Hepatitis C virus.
Viruses; seRNA positive-strand viruses,
Hepacivirus.
NCBI_TaxID=11103;
                                                                                                                                                                                                                                InterPro;
InterPro;
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InterPro;
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InterPro;
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InterPro;
InterPro;
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o; IPR000345; CyrC_heme_BS.
o; IPR001410; DEAD_DEAH N.
o; IPR001552; HCV_capsid..
o; IPR002522; HCV_capsid..
o; IPR002521; HCV_core.
o; IPR002531; HCV_NS1..
o; IPR002531; HCV_NS4a..
o; IPR001490; HCV_NS4a..
o; IPR001490; HCV_NS5a..
o; IPR002166; HCV_RdRP..
o; IPR001030; Peptidase_S29..
o; IPR001030; Peptidase_S29..
o; IPR001030; Peptidase_S29..
o; IPR001031; Peptidase_S29..
o; IPR001031; Peptidase_S29..
o; IPR001031; Peptidase_S29..
o; IPR001031; Peptidase_S29..
o; IPR001040; NNA_DO1_DS_PS..
o; IPR001095; NNA_DO1_DS_PS..
o; IPR001095; NNA_DO1_PSVir..
r01543; HCV_capsid; 1.
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Q901X9
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P90192
P90195
P90195
Q81760
Q94310
Q901X6
Q901X7
Q901X8
Q901X8
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annotation update)
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databases.
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Q9qix9
Q9qiy0
P90192
P90195
P90195
Q683949
Q81310
Q9j310
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Best Local S
Matches 55
                                                                                                                                                                     EMBL; U45476; AAA86507.1; -.
PIR, A61196; A61196.
HSSP; OBJYS1; ICWX.
GO; GO:0016021; C:integral to
GO; GO:0019028; C:viral capsid
GO; GO:0019031; C:viral enveld
GO; GO:000524; F:AIP binding;
GO; GO:0005524; F:AIP-depender
GO; GO:0003723; F:RNA-directee
GO; GO:0003968; F:BNA-directee
GO; GO:0003968; F:serine-type
GO; GO:0005198; F:serine-type
GO; GO:00065198; P:serinctural n
GO; GO:0006509; P:proteolysis
GO; GO:0006509; P:proteolysis
GO; GO:0006509; P:proteolysis
GO; GO:0006509; P:transcripti
GO; GO:0019087; P:viral genome
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01-NOV-1996
01-MAR-2004
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Coat protein; Transmembrane.

SEQUENCE 3010 AA; 327366 MW; D8653F7317FFA106 CRC64.
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Pfam;
Pfam;
Pfam;
Pfam;
Pfam;
Pfam;
                 InterPro;
InterPro;
InterPro;
InterPro;
                                                                       InterPro;
InterPro;
InterPro;
InterPro;
InterPro;
                                                                                                                                                                                                HSSP; OBJYS1; ICWX.

GO; GO:0010021; C:viral cappid; IEA.

GO; GO:0010028; C:viral cappid; IEA.

GO; GO:0010028; C:viral envelope; IEA.

GO; GO:0010031; C:viral envelope; IEA.

GO; GO:0000524; F:ATP-dependent helicase activity; IEA.

GO; GO:0003723; F:RNA binding; IEA.

GO; GO:0003723; F:RNA-directed RNA polymerase activity; IEA.

GO; GO:0003568; F:serine-type peptidase activity; IEA.

GO; GO:0005598; F:structural molecule activity; IEA.

GO; GO:0005598; F:structural molecule activity; IEA.

GO; GO:0006508; P:proteolysis and peptidolysis; IEA.

GO; GO:0006508; P:transcription; IEA.

GO; GO:0019079; P:viral genome replication; IEA.

GO; GO:0019079; P:viral transformation; IEA.
                                                                                                                                            InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
Mueller H.M., Pfaff E., Heller A.E., Goeser T., Theilmar Submitted (JAN-1996) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Polyprotein.
Hepatitis C virus.
Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q68533;
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1; PF01560; HCV_NS1; 1.
1; PF01538; HCV_NS2; 1.
1; PF01038; HCV_NS3; 1.
1; PF010016; HCV_NS4a; 1.
1; PF01001; HCV_NS4b; 1.
1; PF01506; HCV_NS4b; 1.
1; PF01506; HCV_NS4b; 1.
1; PF01506; HCV_NS4b; 1.
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                                                                       IPRO11545;
IPRO11492;
IPRO02522;
IPRO02521;
IPRO02519;
IPRO02519;
IPRO02531;
IPRO0745;
                                             IPR001490;
IPR002868;
                                                                                                                                                                         IPR000345; CytC_heme_BS. IPR001410; DEAD.
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llarity 87.3%;
Conservative
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HCV_RdRP.
Helīcase_C.
Peptidase_S29.
                                           DEAD/DEAH N.
Flavi DEAD.
HCV capsid.
HCV core.
HCV_env.
HCV_NS1.
HCV_NS4a.
HCV_NS5a.
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26,
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Last sequence update)
Last annotation update)
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Pred. No. 1.7e-23;
3; Mismatches 5;
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RESULT 3

G903G8

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Best Local S
Matches 55
R EMBL; AF207765; AAF65955.1; -..

R PIR; A61196, A61196.

R PIR; A61196; A61196.

R PIR; P80329; P80329.

R HSSP; Q8JYSL; 1CWX.

R GO; GO:0016021; C:integral to membrane; IEA.

GO; GO:0019028; C:viral capsid; IEA.

GO; GO:0019031; C:viral envelope; IEA.

GO; GO:0005524; F:ATP-dependent helicase activity; IEA.

GO; GO:00005723; F:RNA-binding; IEA.

GO; GO:00003723; F:RNA-binding; IEA.

GO; GO:0003723; F:RNA-directed RNA polymerase activity; IEA.

GO; GO:0003768; F:RNA-directed RNA polymerase activity; IEA.

GO; GO:0003968; F:structural molecule activity; IEA.

GO; GO:0005198; F:structural molecule activity; IEA.

GO; GO:0005198; F:stranscription; IEA.

R GO; GO:0010379; P:viral genome replication; IEA.

R GO; GO:0010379; P:viral transformation; IEA.

GO; GO:0019087; P:viral transformation; IEA.

R InterPro; IPR001416; DEAD/DEAH N.

R InterPro; IPR0015522; HCV_capsid.
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InterPro; IPR002518; Pept_U39 HCV MS2
InterPro; IPR007095; RNA_Dol_DS_PS_
InterPro; IPR007094; RNA_Dol_DS_PS_
INTERPOST_S; Flavi DEAD; 1.
Pfam; PF01542; HCV_core; 1.
Pfam; PF01542; HCV_core; 1.
Pfam; PF01539; HCV_NS1; 1.
Pfam; PF01539; HCV_NS2; 1.
Pfam; PF01006; HCV_NS3; 1.
Pfam; PF01006; HCV_NS4b; 1.
Pfam; PF01006; HCV_NS4b; 1.
Pfam; PF01006; HCV_NS5a; 1.
Pfam; PF01006; HCV_NS5a; 1.
Pfam; PF00271; HelTcase_C; 1.
Pfam; PF00998; Viral_RdRP; 1.
SMART; SM00487; DEXDG; 1.
SMART; SM00487; DEXDG; 1.
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Q9J3G8;
01-OCT-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nagayama K., Kurosaki M., Er
Submitted (NOV-1999) to the
EMBL; AF207765; AAF65955.1;
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01-OCT-2000 (TrEMBLrel.
01-MAR-2004 (TrEMBLrel.
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Viruses; seRNA positive-strand viruses, no
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=11103;
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nilarity 87.3%;
Conservative
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26,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          nomoto N., Miyasaka Y., Marun
EMBL/GenBank/DDBJ databases.
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Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            UNKNOWN_1.
Glycoprotein; Nonstructural
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NS2.
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2.2e-23;
les 5;
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Best Local S
Matches 54
Nagayama K., Kurosaki M., Enomoto N., Miyasaka Y., Marumo F., Sat.

L Submitted (NOV-1999) to the EMBL/GenBank/DDBJ databases.

R EMBL, AF207762; AAF65952.1; -.

R PIR; A61196; A61196.

R PIR; PS0329; PS0329.

R PIR; PS0329; PS0329.

R PIR; PS0329; C:integral to membrane; IEA.

GO; GO:0016021; C:integral to membrane; IEA.

GO; GO:0019028; C:viral capsid; IEA.

GO; GO:0019031; C:viral envelope; IEA.

GO; GO:0005124; F:ATP-dependent helicase activity; IEA.

GO; GO:0003723; F:RNA binding; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Polyprotein.
HepatitiB C virus.
ViruseB; BBRNA positive-strand viruseB,
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Pfam;
Pfam;
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Pfam;
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InterPro;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Coat protein; Envelope protein; Polyprotein; Transmembrane. SEQUENCE 3010 AA; 326863 MW;
                                                                                                                                                                                                                                                                                                                                                                            STRAIN-MD21;
                                                                                                                                                                                                                                                                                                                                                                                                                                           Hepacivirus.
NCBI_TaxID=11103;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-MAR-2004
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01-OCT-2000
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Coat protein; Envelope protein; Glycoprotein; Nonstructural protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro;
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m; PF01542; HCV_core; 1.
m; PF01539; HCV_env; 1.
m; PF01560; HCV_NS1; 1.
m; PF01503; HCV_NS2; 1.
m; PF01006; HCV_NS4a; 1.
m; PF01001; HCV_NS4b; 1.
m; PF01506; HCV_NS4b; 1.
m; PF01506; HCV_NS4b; 1.
m; PF0151; HelTcase C; 1.
m; PF00998; Viral_RdRP; 1.
m; PF00998; Viral_RdRP; 1.
m; PF00998; Viral_RdRP; 1.
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O; IPR002531; HCV_NS1.
O; IPR002531; HCV_NS1.
O; IPR000745; HCV_NS4a.
O; IPR001490; HCV_NS4b.
O; IPR00166; HCV_NS4b.
O; IPR002166; HCV_RdRP.
O; IPR004109; Peptidase_C.
O; IPR004109; Peptidase_S29.
O; IPR00409003; Pept_U39 HCV_NS2.
O; IPR007095; RNA_Dol_DS_PS.
O; IPR007095; RNA_Dol_DS_PS.
O; IPR007094; RNA_Dol_DS_PS.
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larity 85.7%;
Conservative
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Last annotation update)
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Pred. No. 2.9e-23;
4; Mismatches 5;
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                                                                                                                                                                                                                                                                                                                                                       Sato
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RESULT 5
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POLG_H
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Best Local
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InterPro; IPRO0252; HCV_Capsid.
InterPro; IPRO02521; HCV_Core.
InterPro; IPRO02521; HCV_Core.
InterPro; IPRO02513; HCV_NS4a.
InterPro; IPRO02513; HCV_NS4a.
InterPro; IPRO0268; HCV_NS5b.
InterPro; IPRO01409; HCV_NS5b.
InterPro; IPRO01509; Hellcase C.
InterPro; IPRO01509; Hellcase C.
InterPro; IPRO01509; Peptidase S29.
InterPro; IPRO02518; Pept U39 HCV NS2.
InterPro; IPRO07095; RNA_Dol_DS_PS.
InterPro; IPRO07095; RNA_Dol_DS_PS.
InterPro; IPRO07094; RNA_Dol_DS_PS.
InterPro; IPRO07095; RNA_Dol_DS_PS.
InterPro; IPRO07095; RNA_Dol_DS_PS.
InterPro; IPRO07095; RNA_Dol_DS_PS.
InterPro; IPRO07095; RNA_Dol_PS_Vir.
Pfam; PF01542; HCV_Capsid; 1.
Pfam; PF01543; HCV_Capsid; 1.
Pfam; PF01509; HCV_NS1; 1.
Pfam; PF01509; HCV_NS3; 1.
Pfam; PF01006; HCV_NS4a; 1.
Pfam; PF01006; HCV_NS4a; 1.
Pfam; PF01006; HCV_NS4a; 1.
Pfam; PF01006; HCV_NS5a; 1.
                                                                                                                                                                                      01-AUG-1992 (Rel. 23, Created)
01-AUG-1992 (Rel. 23, Last sequence update)
25-OCT-2004 (Rel. 45, Last sequence update)
25-OCT-2004 (Rel. 45, Last annotation update)
25-OCT-2004 (Rel. 45, Last annotation update)
25-OCT-2004 (Rel. 45, Last annotation update)
25-OCT-2004 (Rel. 45, Last sequence update)
25-OCT-2009 (Rel. 45, Last annotation update)
25-OCT-2009 (Rel. 45, Last annotation update)
26-OCT-2009 (Rel. 45, Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   P26663;
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PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GO; GO:000
GO; GO:000
GO; GO:001
GO; GO:001
InterPro;
InterPro;
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Coat protein; Envelope protein;
Polyprotein; Transmembrane.
SEQUENCE 3010 AA; 327119 MW;
                             SEQUENCE FROM N.A.
MEDLINE=91140698; PubMed=1847440;
                                                                                                                              Hepacivirus.
NCBI_TaxID=11105;
Takamizawa A., Mori C.,
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; GO:0006350;
; GO:0019079;
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IPR001410; DEAD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      86.9%;
nilarity 85.7%;
Conservative
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Fuke I.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 284; DB 2; I
Pred. No. 2.9e-23;
4; Mismatches 5;
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Glycoprotein; Nonstructural
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Manabe
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   Murakami S.,
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   Fujita
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EMBL; M58335; AAA72945.1; -.

PIR; A38465; GNWVTC.

PDB; 1A1Q; X-ray; A/B/C=1027-1215.

PDB; 1C2P; X-ray; A/B=2414-2989.

PDB; 1CSJ; X-ray; A/B=1013-1657.

PDB; 1GX5; X-ray; A/B=1012-1212,

PDB; 1GX5; X-ray; A-B=1027-1212,

PDB; 1GX5; X-ray; A-B=1027-1212,

PDB; 1GX6; X-ray; A-B=1027-1212,

PDB; 1GX6; X-ray; A/B=1027-1212,

PDB; 1GX6; X-ray; A/B=1027-1212,

PDB; 1GX6; X-ray; A/B=1027-1212.

PDB; 1GX6; X-ray; A/B=1027-1212.

PDB; 1GX6; X-ray; A-B=1027-1212.

PDB; 1GX6; X-ray; A-
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"Structure
from human
J. Virol. 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a c between the Swiss Institute of Bioinformatics and the EMBL the European Bioinformatics Institute. There are no restrict use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and foentities requires a license agreement (See http://www.isb-sib.or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -i- FUNCTION: The small proteins NS2A, NS2B, NS4A and NS4B are hydrophobic, suggesting a possible membrane-related function. N and NS5 may play a role in the viral RNA replication.
-i- CATALYTIC ACTIVITY: Hydrolysis of four peptide bonds in the vir precursor polyprotein, commonly with Asp or Glu in the P6 position, Cys or Thr in P1 and Ser or Ala in P1.
-i- CATALYTIC ACTIVITY: N nucleoside triphosphate = N diphosphate +
-i- SUBUNIT: The virion of this virus is a nucleocapsid covered by 11poprotein envelope. The envelope consists of two proteins: protein M and 91ycoprotein E. The nucleocapsid is a complex of protein C and mRNA.
-i- SIMILARITY: Contains 1 peptidase S29 domain.
-i- SIMILARITY: Contains 1 peptidase U39 domain.
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MEDLINE=97015088; PubMed=8861916; DOI=10.1016/S0092-8674(00)81350-1;
LOVE R.A., Parge H.E., Wickersham J.A., Hostomsky Z., Habuka N.,

MOOMBAW E.W., Adachi T., Hostomska Z.;

"The crystal structure of hepatitis C virus NS3 proteinase reveals a trypsin-like fold and a structural zinc binding site.";

Cell 87:331-342(1996).
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MEDLINE=96235224; PubMed=8647104;
Borowski P., Heiland M., Oehlmann
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InterPro; IPR009003; Pept_Ser_Cys.

InterPro; IPR002518; Pept_U39+CV NS2.

R InterPro; IPR002518; Pept_U39+CV NS2.

R InterPro; IPR007095; RNA_pol_DS_PS.

R InterPro; IPR007095; RNA_pol_DS_PS.

R InterPro; IPR007094; RNA_pol_DS_PS.

R InterPro; IPR007094; RNA_pol_DS_PS.

R InterPro; IPR007094; RNA_pol_DS_PS.

R InterPro; IPR007094; RNA_pol_DS_PS.

R Pfam; PF01542; HCV_Capsid; 1.

R Pfam; PF01538; HCV_NS1; 1.

R Pfam; PF01538; HCV_NS2; 1.

R Pfam; PF01006; HCV_NS4a; 1.

R Pfam; PF01006; HCV_NS4a; 1.

R Pfam; PF01006; HCV_NS4a; 1.

R Pfam; PF0156; HCV_NS4a; 1.

R Pfam; PF
CHAIN

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Charge relay system.
Charge relay system.
ATP (Potential).
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N-linked
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Nonstructural protein NS1/E2 (Potential).
Nonstructural protein NS2 (Potential).
Protease/helicase NS3 (Potential).
Nonstructural protein NS4A (Potential).
Nonstructural protein NS4B (Potential).
RNA-directed RNA polymerase (Potential).
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Capsid protein C (Potential).
Matrix protein (Potential).
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Glycoprotein; Helicase;
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SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
FRANTING L.J., Itakura J., Nagg
FRANTING L.J., ITAKURA J., Nagg
Submitted (OCT-2000) to the EI
EMBL, AF313916, AAL55821.1; -
PIR, PQ0246, PP0804.
PIR, PQ0246; PP0804.
PIR, P00804; P00804.
PIR, P00329; P50329.
HSSP, Q93781; ICWX.
GO; GO:0019028; C:viral capsis
GO; GO:0019031; C:viral envel-
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01-MAR-2002 (TrEMBLrel. 20, Last
01-MAR-2004 (TrEMBLrel. 26, Last
Polyprotein (Fragment).
Hepatitis C virus.
Viruses; sBRNA positive-strand v
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01-MAR-2002
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   GO:0016021; C:integral to membrane; GO:0019028; C:viral capsid; IEA. GO:0019031; C:viral envelope; IEA.
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A Nagayama K., Kurosaki M., Enomoto N., Miyasaka Y., Marumo F.

Submitted (NOV-1999) to the EMBL/GenBank/DDBJ databases.

R PER AF207774; AAF65964.1; -.

R PIR; A61196; A61196.

R PIR; P50329; P50329.

R PIR; P50329; P50329.

R PIR; P50329; Civiral capsid; IEA.

GO; GO:0019028; Civiral capsid; IEA.

GO; GO:0019028; Civiral envelope; IEA.

GO; GO:0019028; F:ATP-dependent helicase activity; IEA.

GO; GO:0003733; F:RNA-directed RNA polymerase activity; IEA.

GO; GO:0003968; F:RNA-directed RNA polymerase activity; IEA.

GO; GO:0008236; F:structural molecule activity; IEA.

GO; GO:0008518; F:structural molecule activity; IEA.

R GO; GO:0008518; F:structural molecule activity; IEA.
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Best Local S
Matches 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OR GO: GO:0005524; F:ATP binding; IEA.

RGO: GO:0008026; F:ATP-dependent helicase activity; IEA.

RGO: GO:0003723; F:RNA binding; IEA.

RGO: GO:0003723; F:RNA binding; IEA.

RGO: GO:0003728; F:RNA binding; IEA.

RGO: GO:000326; F:RNA-directed RNA polymerase activity; IEA.

RGO: GO:0008236; F:serine-type peptidase activity; IEA.

RGO: GO:00065198; F:structural molecule activity; IEA.

RGO: GO:00065198; F:structural molecule activity; IEA.

RGO: GO:0006509; P:proteolysis and peptidolysis; IEA.

RGO: GO:0019079; P:viral genome replication; IEA.

RGO: GO:0019079; P:viral genome replication; IEA.

RR GO: GO:0019087; P:viral transformation; IEA.

RR GO: GO:0019087; P:VIRAL transformation; IEA.

RR Pfam; PF01542; HCV_core; 1.

RR Pfam; PF01542; HCV_RS1; 1.

RR Pfam; PF01553; HCV_NS3; 1.

RR Pfam; PF01500; HCV_NS3; 1.

RR Pfam; PF01001; HCV_NS3; 1.

RR Pfam; PF01007; HCV_NS3; 1.

RR Pfam; PF01001; HCV_NS4; 1.

RR Pfam; PF01001; Hclīcase_C; 1.

RR Pfam; PF00999; Viral_RdRP; 1.

RR Pfam; PF00999; Viral_RdRP; 1.

RR Pfam; PF00999; Viral_RdRP; 1.

RR PROSITE; PS00190; CYTOCHROME_C; UNKNOWN_1.

RON_TER 3010 3010

SEQÜENCE 3010 AA; 327182 MW; 33AAA6C07251C839 CRC64;
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Q9J3F9;
01-OCT-2000
01-OCT-2000
01-MAR-2004
                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=MD33;
Nagayama K.,
Submitted (NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hepacivirus.
NCBI_TaxID=11103;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hepatitis C virus.
Viruses; ssRNA positive-strand
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
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nilarity 85.7%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
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15,
26,
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ne EMBL/GenBank/DDBJ databases.
l; -.
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Last sequence update)
Last annotation updat
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Pred. No. 4.8e-23;
3; Mismatches 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 viruses,
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Glycoprotein; Nonstructural
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3010
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RESULT
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Matches
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1410; DEAD

1410; DEAD/DEAH N.

1254; DEAD/DEAH N.

/02522; HCV_capsid.

/02521; HCV_capsid.

/02521; HCV_core.

/02521; HCV_NS1.

PR002531; HCV_NS4.

IPR001450; HCV_NS4A.

IPR001450; HCV_NS4A.

IPR002166; HCV_NS4A.

IPR002166; HCV_RdRP.

/IPR001019; Peptidase S29.

// IPR0010903; Pept_Ser_Gys.

// IPR009003; Pept_Ser_Gys.

// IPR009003; Pept_U39; HCV_NS2.

// IPR007094; RNA_pol_Ds_PS.

// Pro; IPR007095; RNA_pol_Ds_PS.

// Pro; IPR007094; RNA_pol_Ds_PS.

// PR01543; HCV_capsid; 1.

// PP01543; HCV_Capsid; 1.

// PP01538; HCV_NS3; 1.

// Fam; PP01538; HCV_NS3; 1.

// Fam; PP01506; HCV_NS4a; 1.

// PF01506; HCV_NS5a; 1.

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Q9QIX3;
01-MAY-2000
01-MAY-2000
01-MAR-2004
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GO; GO:001
GO; GO:001
InterPro;
InterPro;
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InterPro;
EMBL;
PIR; /
                                               STRAIN=MD9-2;
MEDLINE=20013325; PubMed=10544098; DOI=10.1006
Nagayama K., Kurosaki M., Enomoto N., Maekawa
Tazawa J.i., Izumi N., Marumo F., Sato C.;
"Time-related changes in full-length hepatitis activity.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PROSITE; P800190; CYTOCHROME C; UNKNOWN 1.
Coat protein; Envelope protein; Glycoprotein; Nonstructural protein;
Polyprotein; Transmembrane.
SEQUENCE 3010 AA; 327103 MW; 7162C9DB93E6E0C7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pfam;
Pfam;
Pfam;
Pfam;
Pfam;
Pfam;
Pfam;
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InterPro;
                                 Virology 263:244-253(1999).
                                                                                                                                                                                                            Hepatitis C virus.
Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
                                                                                                                                                                                                                                                               Polyprotein.
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                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                        CBI_TaxID=11103;
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GO:0019079;
GO:0019087;
 ; ĀF165062; AAD
A61196; A61196
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ALEND VVLNAAS VAGSHGILSFLVFF CAAWYIKGRLVFGAAYALYGVWPLLLLLLLALPPR
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                                                                                                                                                                                                                                                                                  (TrEMBLrel. (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                     (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
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                AAD56197.1; -.
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ral transformation;
CytC_heme_BS.
                                                                                                                                                                                                                                                                                  13,
13,
26,
                                                                                                                                                                                                                                                                                Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 282;
Pred. No. 4
                                                                                                                                                                                                                                                                                                                                                        PRT; 3010 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                       DOI=10.1006/viro.1999.9924;
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                                                                    hepatitis C virus
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                                                                                                     s.y.,
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                                                                    and hepatitis
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RESULT
Q98UN3
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Best Local S
Matches 54
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R HSSP; Q8JYS1; 1CWX.

R GO; GO:0016021; C::integral to membrane; IEA.

R GO; GO:0019022; C::viral capsid; IEA.

R GO; GO:0019021; C::viral envelope; IEA.

R GO; GO:000524; F:ATP binding; IEA.

R GO; GO:000825; F:ATP-dependent helicase activity; IEA.

R GO; GO:0003723; F:RNA binding; IEA.

R GO; GO:0003723; F:RNA-directed RNA polymerase activity; IEA.

R GO; GO:0003968; F:RNA-directed RNA polymerase activity; IEA.

R GO; GO:0008258; F:serime-type peptidase activity; IEA.

R GO; GO:0008258; F:serime-type peptidase activity; IEA.

R GO; GO:0008258; F:serime-type peptidase activity; IEA.

R GO; GO:0008259; P:proteolysis and peptidolysis; IEA.

R GO; GO:0006508; P:transcription; IEA.

R InterPro; IPRO11410; DEAD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPRO04109; Peptidase_S29.
InterPro; IPRO09003; Pept Ser Cys.
InterPro; IPRO09003; Pept Ser Cys.
InterPro; IPRO070518; RNA pol DS PS.
InterPro; IPRO07059; RNA pol DS PS.
InterPro; IPRO07094; RNA pol PSVir.
Pfam; PF01543; HCV capsid; 1.
Pfam; PF01543; HCV core; 1.
Pfam; PF01549; HCV NS1; 1.
Pfam; PF01539; HCV_NS1; 1.
Pfam; PF01539; HCV_NS1; 1.
Pfam; PF01586; HCV_NS2; 1.
Pfam; PF01586; HCV_NS3; 1.
Pfam; PF01006; HCV_NS4; 1.
Pfam; PF01006; HCV_NS4; 1.
Pfam; PF01001; HCV_NS4; 1.
Pfam; PF01001; HCV_NS4; 1.
Pfam; PF01001; HCV_NS5a; 1.
Pfam; PF01001; HCV_NS5a; 1.
Pfam; PF01001; HCV_NS5a; 1.
Pfam; PF00098; VIral_RdEP; 1.
SNART; SM00487; DEXDC; 1.
SNART; SM00487; DEXDC; 1.
Polyprotein (Fragm
Hepatitis C virus.
Viruses; ssRNA pos
Hepacivirus.
                                                                                                   Q98UN3;
Q98UN3;
01-JUN-2001
01-JUN-2001
01-MAR-2004
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Polyprotein; T
SEQUENCE 301
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InterPro;
InterPro;
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InterPro;
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InterPro;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      ALENLVVLNAASVAGAHGILSFLVFFCAAWYIKGRLVPGAAYALYGVWPLLLLLLALPSR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ALENLVVLNAASAAGTHGILWFLVFFCAAWYVKGRLVPGATYSLLGLWPLLLLLLLALPQR
                        ssRNA positive-strand
                                                                                                                                                                                                                                                                                                                                                  AYA 809
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1; Transmembrane.
3010 AA; 327254 MW;
                                                                                                   (TrEMBLrel. (TrEMBLrel.
                                                                             (Fragment).
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                                                                                                                                                                                                                  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Envelope protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   86.2%;
85.7%;
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Helicase_C.
                                                                                                      17,
17,
26,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; Score 282; DB ; Pred. No. 4.8e 3; Mismatches
                                                                                                      Last
Last
                                                                                                                                                           Created)
                           viruses,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        UNKNOWN_1.
Glycoprotein; Nonstructural protein;
                                                                                                      sequence update)
annotation update)
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4.8e-23;
6;
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                        DNA stage; Flaviviridae;
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RESULT 10
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Submitted (FEB-2013) to the EMBL/GenBank/DDBJ databases.

EMBL, AF3148705; AAK32686.1; --
REMBL, AF3148705; AAK32686.1; --
REGO; GO:0016021; C:integral to membrane; IEA.
RGO; GO:0019031; C:vital capsid; IEA.
RGO; GO:0019031; C:vital envelope; IEA.
RGO; GO:0005198; F:structural molecule activity; IEA.
R InterPro; IPR002519; HCV env.
R InterPro; IPR002519; HCV S2.
RR InterPro; IPR002531; HCV_NS1.
RR Pfam; PF01539; HCV_NS1; 1.
RR Pfam; PF01539; HCV_NS1; 1.
RR Pfam; PF01539; HCV_NS2; 1.
RR Pfam; PF01539; HCV_NS2; 1.
RR Pfam; PF01539; HCV_NS2; 1.
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Best Local 9
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MEDLINE-21904745; PubMed=11907242;
DOI=10.1128/JV1.76.B.4034-4043.2002;
Kalinina O., Norder H., Mukomolov S., Magn
"A natural intergenotypic recombinant of h
in St. Peteraburg.";
J. Virol. 76:4034-4043 (2002).
EMBL; AV070174; AAL50213.1; -.
HSSP; O91R04; 1BT7.
GO; GO:0019028; C:viral capsid; IEA.
GO; GO:0019031; C:viral envelope; IEA.
                                                                                                                                                                                                                             Q8QP91;
Q8QP91;
01-JUN-2002
01-JUN-2002
01-MAR-2004
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J. Virol. 7
[2]
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NON TER
SEQUENCE
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NON TER
CHAIN
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                                                                                                                                  SEQUENCE FROM N.A.
STRAIN=589;
                                                                                                                                                                  Hepacivirus.
NCBI_TaxID=11103;
                                                                                                                                                                                                      Polyprotein (Fragine Hepatitis C virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A. Chen M.K.C., Hadle
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                                                                                                                                                                                           Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CHAIN
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403
562
AA;
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(TrEMBLrel.
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562
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85.7%;
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Last sequence update)
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97.
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Pred. No. 1.
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                                                                                    Magnius L.O.; of hepatitis C virus identified
                            IEA.
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RESULT 11
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Best Local S
Matches 54
                                   HSSP; QGJYS1; ICWX.

GO; GO:0016021; C:integral to membrane; IEA.

GO; GO:001902B; C:viral capsid; IEA.

GO; GO:0019021; C:viral envelope; IEA.

GO; GO:0005524; F:ATP binding; IEA.

GO; GO:0008526; F:ATP-dependent helicase activity; IEA.

GO; GO:0003723; F:RNA binding; IEA.

GO; GO:0003723; F:RNA directed RNA polymerase activity; IEA.

GO; GO:0003968; F:RNA-directed RNA polymerase activity; IEA.

GO; GO:0008126; F:serine-type peptidase activity; IEA.

GO; GO:0008126; F:serine-type peptidase activity; IEA.

GO; GO:0008128; F:structural molecule activity; IEA.

GO; GO:0006508; F:proteolysis and peptidolysis; IEA.

GO; GO:0006350; P:transcription; IEA.

GO; GO:0006350; P:viral genome replication; IEA.

GO; GO:001907; P:viral transformation; IEA.
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InterPro; IPR002521; HCV_core.
InterPro; IPR002519; HCV_env.
InterPro; IPR002513; HCV_NS1.
InterPro; IPR002513; HCV_NS1.
InterPro; IPR004109; Peptidase S29.
InterPro; IPR004518; Pept_U39 HCV_NS2.
Pfam; PF01543; HCV_capaid; 1.
Pfam; PF01543; HCV_core; 1.
Pfam; PF01549; HCV_NS1; 1.
Pfam; PF01549; HCV_NS3; 1.
Pfam; PF01549; HCV_NS3; 1.
                                                                                                                                                                                                                       Cho M.J.;
Submitted (SEP-1991) to the EMBL/GenBank/DDBJ
EMBL; D14484; BAA03375.1; -.
PIR; A61196; A61196.
PIR; PQ00246; PQ00246.
PIR; PQ00246; PQ00246.
PIR; PQ00246; PQ00246.
PIR; PS0329; PS0329.
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01-NOV-1996 (TrEMBLrel.
01-NOV-1996 (TrEMBLrel.
01-MAR-2004 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                           Hepatitis C virus.
Viruses; ssRNA positive-strand
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             InterPro;
InterPro;
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NCBI_TaxID=11103;
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                                                                                                                                                                                                                                                                                                                 STRAIN=J33;
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                                                                                                                                                                                                                                                                                                                                                                                                           Polyprotein.
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             IPR000345; CytC_heme_BS.
IPR001410; DEAD.
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DEAD/DEAH_N
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Pred. No. 2.6e
3; Mismatches
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RX pubmed=15218169; DOI=10.1099/vir.0.79984-0;

RA Kalinina O., Norder H., Magnius L.O.;

RA Kalinina O., Norder H., Magnius L.O.;

"Full-length open reading frame of a recombinant hepatitis C virus

R train from St Petersburg: proposed mechanism for its formation.";

U. Gen. Virol. 85:1853-1857(2004).

R EMBL; AY587844; AAT00643.1; -.

R GO; GO:0016021; C:integral to membrane; IEA.

R GO; GO:0019028; C:viral capsid; IEA.

R GO; GO:0019031; C:viral capsid; IEA.

R GO; GO:0019031; C:viral envelope; IEA.

R GO; GO:0005524; F:ATP binding; IEA.

R GO; GO:0008026; F:ATP binding; IEA.

R GO; GO:0016723; F:RNA binding; IEA.

R GO; GO:0003723; F:RNA binding; IEA.

R GO; GO:0003723; F:RNA-directed RNA polymerase activity; IEA.
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Best Local S
Matches 54
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PROSITE; PS00190; CYTOCHROME C;
Coat protein; Envelope protein;
POlyprotein; Transmembrane.

SEQUENCE 3010 AA; 327151 MW;
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Pffaam,
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Pfam;
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InterPro;
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InterPro;
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NCBI_TaxID=11103;
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                                                                                                                                                                                                                                               Polyprotein
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PF01506;
PF00271;
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PF01542;
PF01539;
PF01560;
PF01538;
PF02907;
PF02907;
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0; IPR002521; HCV_core.
0; IPR002531; HCV_env.
0; IPR002531; HCV_NS1.
0; IPR001490; HCV_NS4a.
0; IPR0012868; HCV_NS5a.
0; IPR002186; HCV_NS5a.
0; IPR002186; HCV_RS6a.
0; IPR001189; Peptidase_C.
0; IPR004109; Peptidase_S29.
0; IPR0040199; Peptidase_S29.
0; IPR009003; Pept_Ser_Cys.
0; IPR007095; RNA_DOl_DS_ES.
0; IPR007095; RNA_DOl_DS_ES.
0; IPR007095; RNA_DOl_PSVir.
0; IPR007094; RNA_DOl_PSVir.
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HCV_NS1; 1.
HCV_NS2; 1.
HCV_NS3; 1.
HCV_NS4; 1.
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27,
27,
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Last sequence update)
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                                                                                                                                                                                                                        viruses,
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Glycoprotein; Nonstructural
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RESULT 13
Q9DTE1
ID Q9DTE
AC Q9DTE
AC Q9DTE
DT 01-M2
DT 01-M2
DT 01-M2
DT 01-M2
DT Hepac
CX Hepac
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RN [1]
RP SEQUI
RC TISSU
RA Habai
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Best Local S
Matches 54
                                                                          SEQUENCE FROM TISSUE=Serum; Takahashi K.,
                                                                                                                                                                                                                                                                                                                                                           Q9DTE1;
Q9DTE1;
01-MAR-2001
01-MAR-2001
     Hatahara T., Ohta Y., Ke Mishiro S.;
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GO; GO:000
GO; GO:000
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GO; GO:001
InterPro;
                                                                                                                                                                                                                                  Polyprotein.
Hepatitis C virus.
Viruses, SSRNA positive-strand
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InterPro;
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InterPro;
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NCBI_TaxID=11103;
[1]
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InterPro;
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InterPro;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AYA 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ALENLVVLNAASVAGAHGILSFLVFFCAAWYIKGRLVPGAAYALYGVWPLLLLLLALPPR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IPR011545;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IPR001410; DEAD
  C virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                S00190; CYTOCHROME_C; UNKNOWN_1;
g; Coat protein; Envelope protein; Glycoprotein; Helicase;
Nonstructural protein; Polyprotein; Transmembrane.
3010 AA; 326545 MW; D05AB2897F142A58 CRC64;
                                                                                                                                                                                                                                                                                                                              (TrEMBLrel. (TrEMBLrel. (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                      N.A.
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  (HCV)
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HCV_capsid.
HCV_core.
HCV_env.
HCV_NS1.
HCV_NS4a.
HCV_NS5a.
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                                                   Kanai K., Maruo
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16,
26,
genotype
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Last anno
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Pred. No. 6.3e-23;
3; Mismatches 6;
                                                                                                                                                                                                                                                 viruses, no
                                                                                                                                                                                                                                                                                                                                 annotation
                                                                                                                                                                                                                                                                                                                                                              sequence update)
  1b sequences
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                                                   Matsumoto
H., Baba K
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                                                                                                                                                                                                                                                   DNA stage; Flaviviridae;
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  from
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fifteen
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  patients
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RESULT 14
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Best Local S
Matches 54
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InterPro; IPR001345; CyCC heme BS.
InterPro; IPR001545; DEAD/DEAH N.
InterPro; IPR001522; HCV capsid.
InterPro; IPR002521; HCV capsid.
InterPro; IPR002521; HCV capsid.
InterPro; IPR002531; HCV NS4a.
InterPro; IPR002531; HCV NS4a.
InterPro; IPR00140; HCV NS4a.
InterPro; IPR00140; HCV NS4a.
InterPro; IPR001650; HclIcase C.
InterPro; IPR001650; HclIcase C.
InterPro; IPR001650; HclIcase C.
InterPro; IPR001650; HclIcase C.
InterPro; IPR002518; Pept Mase S29.
InterPro; IPR009003; Pept Ser Cys.
InterPro; IPR007094; RNA pol DS PS.
InterPro; IPR007094; RNA pol DS PS.
InterPro; IPR007094; RNA pol PSVir.
Pfam; PF01534; HCV Capsid; 1.
Pfam; PF01539; HCV NS2; 1.
Pfam; PF01539; HCV NS2; 1.
Pfam; PF01506; HCV NS3; 1.
Pfam; PF01006; HCV NS4s; 1.
Pfam; PF01506; HCV NS4s; 1.
Pfam; PF01506; HCV NS4s; 1.
Pfam; PF01506; HCV NS5s; 1.
Pfam; PF00071; HCICASE C; 1.
Pfam; PF000799; VIRAL RGAP; 1.
SMART; SM00487; DESCC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Coat protein;
Polyprotein;
SEQUENCE 30
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Hepatol. Res. 20.161-171(2001).
EMBL; AB049996; BAB18809.1; -.
PIR; A61196; PQ0246.
PIR; PQ0246; PQ0246.
PIR; PQ0252; PQ0252.
PIR; PQ0253; PQ0253.
PIR; PQ0254; PQ0254.
PIR; PQ0804; PQ0804.
PIR; PQ0804; PQ0804.
HSSP; Q8JYS1; 1CMX.
  Q9J3G3
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GO; GO:0019028; C:viral capsid; IEA.
GO; GO:0019031; C:viral envelope; IEA.
GO; GO:0019031; C:viral envelope; IEA.
GO; GO:0005524; F:ATP binding; IEA.
GO; GO:0008026; F:ATP binding; IEA.
GO; GO:0003723; F:RNA-binding; IEA.
GO; GO:0003723; F:RNA-directed RNA polymerase activity; IEA.
GO; GO:0003568; F:RNA-directed RNA polymerase activity; IEA.
GO; GO:0008236; F:serine-type peptidase activity; IEA.
GO; GO:0008236; F:serine-type peptidase activity; IEA.
GO; GO:0008518; F:seructural molecule activity; IEA.
GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
GO; GO:0006508; P:transcription; IEA.
GO; GO:0019087; P:viral genome replication; IEA.
GO; GO:0019087; P:viral genome replication; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ITE; PS00190; CYTOCHROME C; UNKNOWN 1.
protein; Envelope protein; Glycoprotein; Nonstructural protein; Transmembrane.
                                                                                                                                          807
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                                                                                                                                                                                                                                                  ALENLYVLNAASVAGVHGILSFLVFFCAAWYIKGRLVPGAAYALYGVWPLLLLLLALPPR
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  PRELIMINARY;
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85.7%;
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Pred. No. 6.3e-23;
3; Mismatches 6
  PRT;
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Best Local S
Matches 54
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RR PIR; PRO0246; PRO0246.

RR PIR; PRO0246; PRO0246.

RR HSSP; OBJYSI; 1CWX.

GO; GO:0016021; C:integral to membrane; IEA.

GO; GO:0019021; C:viral envelope; IEA.

RGO; GO:0019021; C:viral envelope; IEA.

RGO; GO:0005224; F:ATP-dependent helicase activity; IEA.

RGO; GO:0005236; F:RANA binding; IEA.

RGO; GO:0005236; F:RANA binding; IEA.

RGO; GO:0005198; F:SETUCCUTAL molecule activity; IEA.

RGO; GO:0005198; F:SETUCCUTAL molecule activity; IEA.

RGO; GO:0006508; P:Proteolysis and peptidalysis; IEA.

RGO; GO:0006509; P:transcription; IEA.

RGO; GO:0006509; P:transcription; IEA.

RGO; GO:0006509; P:transcription; IEA.

RGO; GO:0006509; P:transcription; IEA.

RGO; GO:0019087; P:viral genome replication; IEA.

RGO; GO:0019087; P:viral transformation; IEA.

RGO; GO:0019087; PRO0345; CYC Oxee.

RR InterPro; IPR002521; HCV_Cope.

RR InterPro; IPR002521; HCV_NS4.

RR InterPro; IPR002518; Pept_39-HCV NS2.

RR InterPro; IPR003519; RNA_Dol DS PSVIr.

RR InterPro; IPR003519; RNA_Dol DS PSVIr.

RR InterPro; RNA_DOL DS PSVIR.

RR INTERP
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01-OCT-2000
01-OCT-2000
01-MAR-2004
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Submitted (NOV-1999) to the
EMBL; AF207770; AAF65960.1;
                                                                                                                                                                                                                                                                            PROSITE; PS00190; CYTOCHROME C; UNKNOWN 1.
Coat protein; Envelope protein; Glycoprotein; Nonstructu
Polyprotein; Transmembrane.
SEQUENCE 3010 AA; 327227 MW; 19783535650CACE3 CRC64;
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                                                         747
  61
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                                                                                                                                                                    54;
                                                                                                                                                                                              Similarity
  AYA
                                                                                         ALENLVVLNAASAAGTHGILWFLVFFCAAWYVKGRLVPGATYSLLGLWPLLLLLLLALPQR 60
                                                         ALENLVVLNAASVAGAHGILSFLVFFCAAWYIKGRLVPGAAYALYGVWPLLLLLLLALPPR 806
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                                                                                                                                                                    Conservative
  63
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                                                                                                                                                                                           85.9%;
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15,
26,
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1e EMBL/GenBank/DDBJ databases.
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Last sequence up
Last annotation
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••
                                                                                                                                                                 Score 281; DB 2;
Pred. No. 6.3e-23;
3; Mismatches 6
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                                                                                                                                                                                                                                                                                                                                   UNKNOWN_1.
Glycoprotein; Nonstructural
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IEA.

Sato

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Indels

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protein;

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807

AYA

608

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A Nagayama K., Kurosaki M., Enomoto N., Miyasaka Y., Marumo F.

Submitted (NOV-1999) to the EMBL/GenBank/DDBJ databases.

EMBL; AF207767; AAF65957.1; -.

R PIR; A61196, A61196.

R PIR; P80329; P80329.

R PIR; P80329; P80329.

R PIR; P80329; P80329.

R HSSP; OBJYS1; 1CWX.

R MEROPS; S29.002; -.

R GG; GO:0016021; C:integral to membrane; IEA.

GG; GO:0016021; C:viral capsid; IEA.

GG; GO:0019031; C:viral envelope; IEA.

R GG; GO:0008526; F:ATP binding; IEA.

R GG; GO:0008526; F:ATP-dependent helicase activity; IEA.

R GG; GO:0008726; F:ATP-dependent Paper Comparase activity; IEA.

R GG; GO:0008726; F:RNA-directed RNA polymerase activity; IEA.

R GG; GO:0008726; F:serine-type peptidase activity; IEA.

R GG; GO:0008269; F:structural molecule activity; IEA.

R GG; GO:0008596; F:structural molecule activity; IEA.

R GG; GG:0008596; F:structural molecule activity; 
Pfam; PF01543; HCV capsid; 1.

Pfam; PF01542; HCV core; 1.

Pfam; PF01539; HCV env; 1.

Pfam; PF01560; HCV NS1; 1.

Pfam; PF01560; HCV NS2; 1.

Pfam; PF01006; HCV NS4; 1.

Pfam; PF01006; HCV NS4; 1.

Pfam; PF01006; HCV NS5a; 1.

Pfam; PF00271; Helīcase C; 1.

Pfam; PF00271; Helīcase C; 1.

SMART; SM00487; DEXDC; 1.

SMART; SM00487; DEXDC; 1.

PROSITE; PS00190; CYTOCHROME C; UNKNOWN 1.

Coat protein; Envelope protein; Glycoprotein; Nor
                                                                                                                                                                                                                                                                        InterPro;
Pfam; PFO;
Pfam; PFO;
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InterPro;
InterPro;
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01-OCT-2000
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InterPro;
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InterPro;
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01-MAR-2004
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Hepatitis C
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NCBI_TaxID=11103;
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                                                                                                                                                                                                                                                                                                      o; IPR011545; DEAD/DEAH N.
c; IPR01252; HCV capsid.
c; IPR002521; HCV capsid.
c; IPR002521; HCV cenv.
c; IPR002531; HCV NS1.
c; IPR002531; HCV NS1.
c; IPR00245; HCV NS4b.
c; IPR002466; HCV NS5a.
c; IPR002166; HCV NS5a.
c; IPR002166; HCV NS5a.
c; IPR001650; Helicase C.
c; IPR004109; Peptidase S29.
c; IPR004019; Pept Ser Cys.
c; IPR007095; RNA DOL DS PS.
c; IPR007095; RNA DOL PSVIr.
c; IPR007094; RNA DOL PSVIr.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               o; IPR000345; CytC_heme_BS.
j; IPR001410; DEAD.
j; IPR01545; DEAD/DEAH N.
j; IPR002522; HCV_capsid.
j; IPR002521; HCV_core.
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